



SEQUENCE LISTING

<11> Rhodes, Kenneth
Betty, Maria
Ling, Hui-Ping
An, Wenqian

<12> POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR

<13> MNI-070CP4

<14> USPN 04/070,756
<141> 2004-09-27

<15> USPN 04/110,277
<151> 1994-11-10

<15> USPN 04/110,033
<151> 1994-11-05

<15> USPN 04/109,333
<151> 1994-11-01

<15> USPN 04/106,731
<151> 1994-04-25

<15> USPN 04/050,614
<151> 1994-07-09

<15> USPN 04/050,874
<151> 1994-07-09

<15> USPN 04/040,492
<151> 1994-04-11

<15> USPN 04/089,913
<151> 1994-09-21

<15> PCT/US94/17428
<151> 1994-11-19

<16> 53

<17> PatentIn Ver. 1.1.0

<21> 1
<211> 146
<212> DNA
<213> Homo sapiens

<214>
<215> CDS

atg ggc acc ttc tca tct ctg caa acc aaa caa agg cga gcc tgg aaa 284
Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg Arg Pro Ser Lys
5 10 15 20

gat aag att gaa gat gag ctg gag atg aac atg gtt tgc cat cgg ccc 332
Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys His Arg Pro
25 30 35

gag gga ctg gag gag ctg gag gcc gag aac aac ctg aac aag agg gag 380
Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg Glu
40 45 50

ctg cag gtc att tat cga gcc ttc aaa aat gag tgc ccg agt ggt gtg 428
Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val

55 60 65

gtc aac gaa gac aca ttc aag cag atc tat gct cag ttt ttc ccc cat 476
Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His
70 75 80

gga gat ggc agc aag tat gcc cat tgc ctc ttc aat gcc ttc gac acc 524
Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr
35 30 35 100

act gag aca ggc ttc gtc aag ttc gag gac ttt gta aac gct ctg tag 572
Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser
105 110 115

att tta ttg aga gga ast gtc cac gag aaa cta agg tgg aca ttt aat 620
Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn
120 125 130

tig tat gac atc aac aag gac gga tac ata aac aaa gag gag atg atg 668
Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met
 135 140 145

gac att gtc aaa ggc atc tac gac atg atg ggg aaa tac aaa tat cgt 116
Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro
150 155 160

PPT TTT AAA GAG GAC ACT CCG AGG CAG CAT GTG GAC GTC TTC TTC CAG 764
 Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln
 165 170 175 180

aaa atg tac aaa aat aaa gat ggc atc gta gct tta aa' gaa ttt ctt 410
Lys Met Asp Lys Asp Lys Asp Gly Ile Val Thr Leu Asn Glu Phe Leu
185 190 195

tactaaacaa	caacttaac	acootgatet	gcoettgtte	tgatttara	caacaaet et	912
tgggacagaa	acacotttta	caotttggaa	gaattototg	ctgaagactt	tottatggaa	1031
cccagpatca	tgtgggtcag	tctotgattg	ccaactotte	ctotttotte	ttottgagag	1092
agacaagatg	aaatttgayt	ttgttttggg	agcatgetca	tctectcaca	ctgetgcoot	1152
atggaaggte	cctctgetta	agettaaaca	gtagtgcaca	aaatatgetg	cttaegtgc	1212
cccagcccac	tgootccaag	ccaggcagac	cttgggtgaat	ctggaagcaa	gaggacotga	1272
gcccagatgca	caccatctct	gatggootcc	caaaccaatg	tgcotgttte	tottcctttg	1332
gtgggaagaa	tgagagttat	ccagaacaaat	taggatctgt	catgaccaga	ttgggagagc	1392
cagcactaa	catatgtggg	ataggactga	attattaagc	atgacattgt	ctgatgaccc	1452
aaactgcctcc	g					1463

```

0210. 2
0211. 216
0212. PRT
0213. Homo sapiens

```

[illegible]

Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
180 185 190

Asp Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser
195 200 205

Leu Gln Leu Phe Gln Asn Val Met
210 215

<210> 3

<211> 1856

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (300)..(1034)

<400> 3

ggcagacacac cccctggallc ttccggagaat atgcccgtgag gtgttgccaa ttattagtto 60

tcttggtctag cagatgttta gggactgggtt aagccttttg agaaattacc ttaggaaaaac 120

ggggaaataa aagcaagat taccatgaat tgcaagatta cctagcaatt gcaaggtagg 180

agqagagagg tggaggggcgg agtagacagg agggaggggag aaagtgagag gaagctaggc 240

tggtygaaat aacccctgcac ttggaacagc ggcaagaagc ccgcatcttc cagctttaa 299

atg cct gcc cgc gtt ctg ctt gcc tac ccg gga acg gag atg ttg acc 347

Met Pro Ala Arg Val Leu Leu Ala Tyr Pro Gly Thr Glu Met Leu Thr
1 5 10 15

cag gcc gag tct gaa ggg ctc cag acc ttg ggg ata gta gtc gtc ctg 395

Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu
20 25 30

ctt tcc tct ctg aaa cta ctg cac tac ctc ggg ctg att gac ttg tcc 443

Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
35 40 45

gat gac aag atc gag gat gat ctg gag atg acc atg gtc tgc cgt cgg 491

Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg
50 55 60

ttt ttt ggt ctg gag cag ctt gag gca cag acc aac ttc acc aag aga 539

Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg
65 70 75 80

gaa ctg caa gtc ctt tac cgt gga ttc aaa aac gag tgc cgt att ggt 597

Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
85 90 95

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 657

Met Met Met Met Met Met Met Met Met Met Met Met Met Met Met Met

<210> 4
 <211> 245
 <212> IRT
 <213> Rattus sp.

<400> 4

Met	Pro	Ala	Arg	Val	Leu	Leu	Ala	Tyr	Pro	Gly	Thr	Glu	Met	Leu	Thr
1				5					10					15	
Gln	Gly	Glu	Ser	Glu	Gly	Leu	Gln	Thr	Leu	Gly	Ile	Val	Val	Val	Leu
			20					25					30		
Cys	Ser	Ser	Leu	Lys	Leu	Leu	His	Tyr	Leu	Gly	Leu	Ile	Asp	Leu	Ser
	35						40					45			
Asp	Asp	Lys	Ile	Glu	Asp	Asp	Leu	Glu	Met	Thr	Met	Val	Cys	His	Arg
	50					55					60				
Pro	Gln	Gly	Leu	Glu	Gln	Leu	Glu	Ala	Gln	Thr	Asn	Phe	Thr	Lys	Arg
65					70					75					80
Glu	Leu	Gln	Val	Leu	Tyr	Arg	Gly	Phe	Lys	Asn	Glu	Cys	Pro	Ser	Gly
			85						90						95
Val	Val	Asn	Glu	Glu	Thr	Phe	Lys	Gln	Ile	Tyr	Ala	Gln	Phe	Phe	Pro
			100					105					110		
His	Gly	Asp	Ala	Ser	Thr	Tyr	Ala	His	Tyr	Leu	Phe	Asn	Ala	Phe	Asp
	115						120					125			
Thr	Thr	Gln	Thr	Gly	Ser	Val	Lys	Phe	Glu	Asp	Phe	Val	Thr	Ala	Leu
	130					135					140				
Ser	Ile	Leu	Leu	Arg	Gly	Thr	Val	His	Glu	Lys	Leu	Arg	Trp	Thr	Phe
145					150					155					160
Asn	Leu	Tyr	Asp	Ile	Asn	Lys	Asp	Gly	Tyr	Ile	Asn	Lys	Glu	Glu	Met
			165					170					175		
Met	Asp	Ile	Val	Lys	Ala	Ile	Tyr	Asp	Met	Met	Gly	Lys	Tyr	Thr	Tyr
			180					185					190		
Pro	Val	Leu	Lys	Glu	Asp	Thr	Pro	Arg	Gln	His	Val	Asp	Val	Phe	Phe
	195						200					205			
Gln	Lys	Met	Asp	Lys	Asn	Lys	Asp	Gly	Ile	Val	Thr	Leu	Asp	Glu	Phe
	210					215					220				
Leu	Glu	Ser	Cys	Gln	Glu	Asp	Asp	Asn	Ile	Met	Arg	Ser	Leu	Gln	Leu
225					230					235					240
Phe	Gln	Asn	Val	Met											

1
 117
 118

<220>

<221> CDS

<222> (477)..(1124)

<400> 5

cggccccctg agatccagcc cagagcgagg gaggagcggc cgggtggcag cagggggggg 60
 cggggcggagc gaagctcccg caccgcacgc ggccggggct cggcagccct ggccgtggcg 120
 gcacgcgggc ccagtgtcca acatcaggca ggttttgggg ctgggggctc ggccctcgga 180
 gaagccagtg gcccggctgg gtgcgcgac cggggggcgc ctgtgaagc tcccgcgagc 240
 ctctggccct gggagtcagt gaatgtgact ggtgaagaa ggcagcagc acgagctcca 300
 ggagcccggg cccacgctt ttggaatac aagctgcagg cagctgtctc ggggcttttt 360
 tgctttctcg cttttctct cctccaatc aaagtgggca atccacacg attttttt 420
 aggggagggg agagacagg cctggggctc caagacccac acaagtttc gtgccc atg 479
 Met
 1

ggg gcc gtc atg ggc act ttc tcc tcc ctg cag acc aaa caa agg cga 527
 Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg Arg
 5 10 15

ccc tct aaa gac aag att gag gat gag cta gag atg acc atg gtt tgc 575
 Pro Ser Lys Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys
 20 25 30

cac cgg cct gag gga ctg gag cag ctt gag gca cag acc aac ttc acc 625
 His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr
 35 40 45

aag aga gaa ctg caa gtc ttg tac cgg gga ttc aaa aac gag tgc cct 671
 Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro
 50 55 60 65

agc ggt gtg gtc aat gaa gaa aca ttc aag cag atc tac gct cag ttt 719
 Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe
 70 75 80

ttc cct cac gga gat gct agc aca tat gca tat tac ttc ttc aat gct 767
 Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Ile Asn Ala
 85 90 95

ttc gac acc acc cag aca ggc tct gta aag ttc gag gac ttt gtg act 815
 Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr
 100 105 110

att ctg tgg att ttc ctg aga ggg aca gtc cat gaa aaa cta agg tga 863
 Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Ile Leu Ile Thr Leu

gag atg atg gac ata gtc aaa ggc atc tat gac atg atg ggg aaa tac 959
 Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr
 150 155 160

acc tat cct gtg ctc aaa gag gag act acc agg cag cat gtg gat gtc 1009
 Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val
 165 170 175

ttc ttc cag aaa atg gat aaa aat aaa gat ggc att gta acg tta gat 1055
 Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp
 180 185 190

gaa ttt ctt gaa tca tgt cag gag gat gac aac atc atg aga tct cta 1103
 Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu
 195 200 205

cag ctg ttc caa aat gtc atg taactgagga cactggccat tctgctctca 1154
 Gln Leu Phe Gln Asn Val Met
 210 215

gagacactga caaacacott aatgcctga tctgccttg ttcacatttt acacaccaac 1214

tcttgggaga gaaatcctt ttacactttg gaagaattct ctgttgaaga ctttctacaa 1274

aacctggcac caagtggctc tgtctctgag ggaacgaggg agatccgact ttgttttgga 1334

agcatgcaca tctcttcctg ctgttgcctt gtggaaggcc cctctgcttg agcttaatca 1394

atagtgcaca gttttatgct taacatatat cccaaactcac tgcctccaag tcaggcagac 1454

tctgatgaat ctgagccaaa tgtgcacct cctccgatgg cctcccaagg caatgtgctt 1514

gctctctctt cctctggtggg aagaaagagt gttctacgga acaattagag cttaccatga 1574

aaatattggg agaggcagca cctaaccat gtagaatagg actgaattat taagcatggt 1634

gatatcagat gatgcacatt gcccatgcca tttttttcaa aggtaggggac aaatgattct 1694

cccacactag cactgttggt catagagcaa gtctcttaac atgcccagaa ggggaaccac 1754

tgtccagtgg tctatccctt ctctccatcc cctgtctaaa cccagcactg catgtccttc 1814

caagaangtc cagaatgctt ccccaacgct gtaatttat aactgttct acttaataaa 1874

caacacactt tcttcaaaa caacacacac aa 1934

<210> 6

<211> 216

<212> FRT

<213> Mus musculus

<400> 6

lys his asp thr thr thr thr thr thr thr thr thr thr thr thr thr thr thr

Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
50 55 60

Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln
65 70 75 80

Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
85 90 95

Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
100 105 110

Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg
115 120 125

Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
130 135 140

Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
145 150 155 160

Tyr Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp
165 170 175

Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
180 185 190

Asp Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser
195 200 205

Leu Gln Leu Phe Gln Asn Val Met
210 215

<10> 7

<11> 1534

<12> DNA

<13> Rattus sp.

<120>

<121> CDS

<122> (31)..(711)

<123>

Met Gly Ala Val Met Gly Thr Phe
1 5

tgg tcc ctg cag acc aaa caa agg cga ccc tcc aaa gag atc ggc tgg 100
Ser Ser Leu Gln Thr Lys Gln Arg Arg Pro Ser Lys Asp Ile Ala Trp
10 15 20

Met Val Tyr His Arg Ile Val Lys Arg Val Val Leu His Ala Gln
25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100

acg aac ttc acc aag aga gaa atg caa gtc att tac cgg gga ttc aia 240
Thr Asn Phe Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys
60 65 70

aac gag tgc ccc agt ggt gtg gtt aac gaa gag aca ttc aag cag atc 294
Asn Glu Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile
75 80 85

tac gct cag ttt ttc cct cat gga gat gcc agc aca tac gca cat tac 342
Tyr Ala Gln Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr
90 95 100

ctc ttc aat gcc ttc gac acc acc cag aca ggc tct gta aag ttc gag 390
Leu Phe Asn Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu
105 110 115 120

gac ttt gtg act gct ctg tgg att tta ctg aga gga acg gtc cat gaa 438
Asp Phe Val Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu
125 130 135

aac ctg agg tgg aac ttt aat ttg tac gac atc aat aaa gac ggc tac 486
Lys Leu Arg Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr
140 145 150

ata aac aaa gag gag atg atg gac ata ggc aaa gcc atc tat gac atg 534
Ile Asn Lys Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met
155 160 165

atg ggg aaa tac acc tat cct gtg ctg aaa gag gac act ccc agg cag 582
Met Gly Lys Tyr Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln
170 175 180

cac gtg gac gtc ttc ttc cag aaa atg gat aaa aat aaa gat ggc att 630
His Val Asp Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile
185 190 195 200

gta acg tta gac gaa ttt ctg gag tcc tgt cag gag gat gac aac atc 678
Val Thr Leu Asp Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile
205 210 215

atg agg tct cta cag ctg ttc caa aat gtc atg taactgagga cactggccat 731
Met Arg Ser Leu Gln Leu Phe Gln Asn Val Met
220 225

acgtgctctcag gacacattca caaacattc atggttca tcttctctcag tcttctctcag 761

cttctctcag tcttctctcag caaataccct ttacacttct caaggaattct ctgtctgaaga 851

cttctctcag caactctgcaag cggctggctc agtctctgat tgcacacattc tcttctctcag 911

tcttctctcag aggaacagag tcaaatcaga atttctctcag tcttctctcag cactctcag 971

atgtctctcag tcttctctcag caaacattc atggttca tcttctctcag tcttctctcag 1031

acgtgctctcag gacacattca caaacattc atggttca tcttctctcag tcttctctcag 1091

cttctctcag tcttctctcag caaataccct ttacacttct caaggaattct ctgtctgaaga 1151

cttctctcag caactctgcaag cggctggctc agtctctgat tgcacacattc tcttctctcag 1211

caaacagccc atgtcatttt ttttccagag gtagggacta ataattctcc cacactagca 1331
 cctacgatca tagaacaagt cttttaaac atccaggagg gaaacgctg ccagtggtc 1391
 tctcccttct ctccatccc tgcctaaagc cagcactgca tgtctctccc ggaaggcca 1451
 gaatgcctgt gaaatgctgt aacttttata cccgtgtata atcaataaac agaactattt 1511
 cgtacaaaaa aaaaaaaaaa aaa 1534

<210> 8

<211> 227

<212> PRT

<213> Rattus sp.

<400> 2

Met	Gly	Ala	Val	Met	Gly	Thr	Phe	Ser	Ser	Leu	Gln	Thr	Lys	Gln	Arg
1				5						10				15	
Arg	Pro	Ser	Lys	Asp	Ile	Ala	Trp	Trp	Tyr	Tyr	Gln	Tyr	Gln	Arg	Asp
			20					25					30		
Lys	Ile	Glu	Asp	Asp	Leu	Glu	Met	Thr	Met	Val	Cys	His	Arg	Pro	Glu
		35					40					45			
Gly	Leu	Glu	Gln	Leu	Glu	Ala	Gln	Thr	Asn	Phe	Thr	Lys	Arg	Glu	Leu
	50					55					60				
Gln	Val	Leu	Tyr	Arg	Gly	Phe	Lys	Asn	Glu	Cys	Pro	Ser	Gly	Val	Val
65					70				75					80	
Asn	Glu	Glu	Thr	Phe	Lys	Gln	Ile	Tyr	Ala	Gln	Phe	Phe	Pro	His	Gly
				85					90					95	
Asp	Ala	Ser	Thr	Tyr	Ala	His	Tyr	Leu	Phe	Asn	Ala	Phe	Asp	Thr	Thr
			100					105					110		
Gln	Thr	Gly	Ser	Val	Lys	Phe	Glu	Asp	Phe	Val	Thr	Ala	Leu	Ser	Ile
		115					120					125			
Leu	Leu	Arg	Gly	Thr	Val	His	Glu	Lys	Leu	Arg	Trp	Thr	Phe	Asn	Leu
	130					135					140				
Tyr	Asp	Ile	Asn	Lys	Asp	Gly	Tyr	Ile	Asn	Lys	Gln	Gln	Met	Met	Asp
145				150						155					160
Ile	Val	Lys	Ala	Ile	Tyr	Asp	Met	Met	Gly	Lys	Tyr	Thr	Tyr	Pro	Val
			165						170					175	
Leu	Lys	Gln	Asp	Thr	Pro	Arg	Gln	His	Val	Asp	Val	Phe	Phe	Gln	Lys
			180				185								

11
 11
 11

t.t.c

at g
Met

a c
q p

g a
s t

a c
y l

a g
n v

t g
n G

t g
p A

Y. 11

a c
u l

• 7

acc tat cct gtg ctc aaa gag gac agt ccc agc cag cat gtg gat gtc 642
 Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val
 175 180 185

ttc ttc cag aaa atg gat aaa aat aaa gat ggc att gta acg tta gat 658
 Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp
 190 195 200

gaa ttt ctt gaa tca tgt cag gag gat gac aac atc atg aga tct cta 736
 Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu
 205 210 215 220

cag ctg ttc caa aat gtc atg taactgagga cactggccat tctgctctca 787
 Gln Leu Phe Gln Asn Val Met
 225

gagacactga caaacacott aatgccttga tctgccttg ttccaatttt acacaccaac 847
 tottgggaca gaaatacott ttacaotttg gaagaattct ctgctgaaga ctttctacaa 907
 aacctggcac cagtggttc tctctctgag ggaagagagg agatccgact ttgttttga 967
 agcatgcaca tctcttcctg ctgctgacct gtggaaggcc cctctgcttg agcttaacca 1027
 atagtgcaca gttttatgct tacacatata cccaactcac tgcctccaag tcaggcagac 1087
 tctgatgaat ctgagccaaa tctgcacct cctccgatgg cctcccaagg caatgtgctt 1147
 gcttctcttc ccttggttgg aagaaagagt gttctacgga acaattagag cttaccatga 1207
 aatatattgg agaggcagca cctaacacat gtagaatagg actgaattat taagcatggt 1267
 gatatacagat gatgcacatt ggcctatgta tttttttcaa aggtagggac aaatgattct 1327
 cccacactag cactgttggc catagagcaa gtctcttaac atgccacaga ggggaaccac 1387
 tgtccagtgg tctatccctc ctctccatcc cctgctcaaa cccagcactg catgtccctc 1447
 caagaaggtc cagaatgctt gogaaaagct gtacttttat acctgtttct aatcaataaa 1507
 cagaactatt tctacaaaa aaaaaaaaaa aaa 1540

<210> 10
 <211> AAT
 <212> FRT
 <213> Mus musculus

<400> 10
 Met Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg
 1 5 10 15

Arg Pro Ser Lys Asn Ile Ala Thr Tyr Thr Thr Ala Thr Thr Thr Thr

Arg Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr
 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100

Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val Val
65 70 75 80

Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His Gly
85 90 95

Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr Thr
100 105 110

Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser Ile
115 120 125

Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn Leu
130 135 140

Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met Asp
145 150 155 160

Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Val
165 170 175

Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln Lys
180 185 190

Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe Leu Glu
195 200 205

Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu Phe Gln
210 215 220

Asn Val Met
225

<110> 11
<111> 955
<112> DNA
<113> Rattus sp.

<220>
<221> CDS
<222> (345)..(953)

<223>
<224> misc feature
<225> 619
<226> aa,c,g, or t

<227>
<228> VARIANT
<229> 92 of the corresponding amino acid
<230> X-ray amino acid

ataggatggt ggaaataaac ctgcacttgg aacagaggca aagaagggg attttorago 307
 tttaaatgac tgcacgggtt ctgcttggct acccggggaac ggag atg ttg acc gag 356
 Met Leu Thr Sin
 1
 ggc gag tct gaa ggg ctg cag acc ttg ggg ata gta gtg gtc ctg tgt 404
 Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu Cys
 5 10 15 20
 tcc tct ctg aaa cta ctg cac tac ctg ggg ctg att gac ttg tgg gat 452
 Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser Asp
 25 30 35
 gac aag atc gag gat gat ctg gag atg acc atg gtt tgc cat cgg cct 500
 Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg Pro
 40 45 50
 gag gga ctg gag cag ctt gag gca cag acg aac ttc acc aag aga gaa 548
 Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg Glu
 55 60 65
 ctg caa gtc ctt tac cgg gga ttc aaa aac gag tgc ccc agt ggt gtg 596
 Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val
 70 75 80
 gtt aac gaa gag aca ttc aag cng atc tac gct cag ttt ttc cct cat 644
 Val Asn Glu Glu Thr Phe Lys Xaa Ile Tyr Ala Gln Phe Phe Pro His
 85 90 95 100
 gga gat gcc agc aca tac gca cat tac ctg ttc aat gcc ttc gac acc 692
 Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr
 105 110 115
 acc cag aca ggc tct gta aag ttc gag gac ttt gtg act gct ctg tgg 740
 Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser
 120 125 130
 att tta ctg aga gga acg gtc cat gaa aaa ctg aag tgg acg ttt aat 788
 Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys Trp Thr Phe Asn
 135 140 145
 ttg tac gac atc cat aaa gac ggc tac ata aac aaa gag gtt atg atg 836
 Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Gln Gln Met Met
 150 155 160
 gac ata gtg aaa gcc atc tat gac atg atg ggg aaa tac acc tat ctt 884
 Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Leu
 165 170 175 180
 gta ctg aaa gag ttt atc ttc agt tgg caa ttg gtt gtt ttc ttc cag 932
 Val Leu Lys Glu Asp Thr Ser Arg Gln His Val Arg Thr Thr Thr Thr

<211> 203
<212> PRT
<213> Rattus sp.

<220>
<221> VARIANT
<222> 92
<223> Xaa=any amino acid

<400> 12
Met Leu Thr Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val
1 5 10 15
Val Val Leu Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile
20 25 30
Asp Leu Ser Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val
35 40 45
Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
50 55 60
Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
65 70 75 80
Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Xaa Ile Tyr Ala Gln
85 90 95
Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
100 105 110
Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
115 120 125
Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys
130 135 140
Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
145 150 155 160
Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
165 170 175
Tyr Thr Tyr Leu Val Leu Lys Glu Asp Thr Ser Arg Gln His Val Asp
180 185 190
Val Thr Phe Gln Lys Met Asp Lys Asn Lys Asp
195 200

<210> 13
<211> 1334
<212> RNA

cct gga ctc cgg gag gag gcc cca agg gaa caa atg gag agc ttc ttc 908
 Pro Ala Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe
 220 225 230

cag aag atg gac aga aac aag gat ggt gtg gtg acc att gag gaa ttc 953
 Gln Lys Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe
 235 240 245

att gag tct tgt caa aag gat gag aac atc atg agg tcc atg gag ctc 1001
 Ile Glu Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu
 250 255 260 265

ttt gac aat gtc atc tagcccccag gagagggggg cagtgtttcc tgggggggacc 1056
 Phe Asp Asn Val Ile
 270

atgctctaac cctagtcacag ggggaacctca cccctctctt cccaggctca tcttcactct 1116
 acgcctccct gggggctgga gggatccaaag agcttggggga ttcagtagtc cagatctctg 1176
 gagctgaagg ggcacagagag tgggcagagt gcctctcggg ggggtgttccc aactcccacc 1236
 agctctcacc cccctctctg ctgacaccca gtgttgagag tgcctctctt gtaggaattg 1296
 agcgggtccc cactctctac cctactctag aaacacacta gagcgatgtc tctgctatg 1356
 gtgcttcccc catcctgac ctacataaaca ttcccccata gactcccttc tcagagagaa 1416
 tctctccttc tgggaactgg ctggctcttc agaccagcca ttgagagccc tgtgggaggg 1476
 ggacaagaat gtatagggag aaatcttggg cctgagtcac tggataggtc ctaggaggtg 1536
 ggtgggggtt agaatagaag ggcttggaac gattatgatt gctcaggaat accaggttat 1596
 agctccaagt tccacaggtc tctacacaca ggccatcaaa atataagttt ccaggctttg 1656
 cagaagacct tgtctcctta gaaatgcctc agaaaatttc cacacccttc tgggtatcca 1716
 tggagagcct ggggcacagat atctggtcca tctctggcat tgcctctctt ccttctcttc 1776
 tgcctgtgtt ggtggtggtt gtggtggggg aatgtggatg ggggatgttc tgctgatgc 1836
 ctgcaaaat tctatccac cctccttctt tctctctctt gtttgggg ctatgacttg 1896
 gtttctct tctctctctt tctctctctt tctctctctt tctctctctt tctctctctt 1956
 tctctctctt ggtatgctta gaaggagag agaaaggagg aggcaggaat agc 2009

<210> 14

<211> 277

<212> 187

<213> 187

Arg Gly Ser Lys Arg Ser Ser Thr Lys His Leu Ile Lys Ile Thr Lys

Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro Ala Ser Leu
 50 55 60
 Arg Pro His Arg Pro Arg Leu Leu Asp Pro Asp Ser Val Asp Asp Glu
 65 70 75 80
 Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu
 85 90 95
 Gln Glu Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg
 100 105 110
 Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe
 115 120 125
 Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr
 130 135 140
 Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val
 145 150 155 160
 Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr
 165 170 175
 Val Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys
 180 185 190
 Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile
 195 200 205
 Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala
 210 215 220
 Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys
 225 230 235 240
 Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp
 245 250 255
 Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 260 265 270

<210> 15
 <211> 1247
 <212> 1NA
 <213> *Battus* sp.

<220>
 <221> 333

... ..

Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys	
20 25 30	
tgc ggg ccc caa gcc ctg ccc tca gtc agt gaa aca tta gct gcc cca	145
Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro	
35 40 45	
gcc tcc ctg agc ccc caa aga ccc cgc ccg ctg gac cca gac agc gta	193
Ala Ser Leu Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val	
50 55 60	
gag gat gag ttt gaa tta tcc acg gtg tgt cac cga cct gag ggc ctg	241
Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu	
65 70 75 80	
gaa caa ctc cag gaa cag acc aag ttc aca cgc aga gag ctg cag gtc	289
Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val	
85 90 95	
ctg tac cga ggc ttc aag aac gaa tgc ccc agt ggg att gtc aac gag	337
Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu	
100 105 110	
gag aac ttc aag cag att tat tct cag ttc ttt ccc caa gga gac tcc	385
Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser	
115 120 125	
agc aac tat gct act ttt ctg ttc aat gcc ttt gac acc aac cac gat	433
Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp	
130 135 140	
ggc tct gtc agt ttt gag gac ttc ggc gct ggt ttg tgg gtc att ctt	481
Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu	
145 150 155 160	
cgg ggg acc ata gat gat aga ctg agc tgg gct ttc aac tta tat gac	529
Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp	
165 170 175	
ctc aac aag gac ggc tgt atc aca aag gag gaa atg ctt gac att atg	577
Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met	
180 185 190	
aag tcc atc tat gac atg atg ggc aag tac aca tac ccc gtc ctg cgg	625
Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg	
195 200 205	
gag gag ggc cca aga gaa caa ggc gag agc ttc ttc cag aag atg gac	673
Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp	
210 215 220	
agg aac aag gac ccc atc atg acc atc gag gaa ttc atc gag tct ttt	721
Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys	
225 230 235	

tccatgctca gacgaacctc accctctctc tccaggcttg tcccatctt accgtgacct 982
 tgggggctgt agggattcaa taccctgggg ctccagtagt ccagatccct gagctaagtc 942
 acaaaagtag gcaagagtag gcaagctaaa tctggggggt tcccaacccc ccagagctct 1002
 caccctctct caactgatac ctagtgtgga ggaacacct ggtgtaggga ccaagtgggt 1062
 ctccaccttc tagtcccact ctagaaacca cattagacag aaggtctcct gctatgggtc 1122
 ttcccccata cctaattctt tagattttcc tcaagactcc ctctccagag aacacgctct 1182
 gtccatgtcc ccagctgggg acatggacag agcgtgttct ctagttctag atcgcgagcg 1242
 gcgcg 1247

<210> 16
 <211> 257
 <212> PRT
 <213> Rattus sp.

<400> 16
 Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly
 1 5 10 15
 Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys
 20 25 30
 Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro
 35 40 45
 Ala Ser Leu Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val
 50 55 60
 Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
 65 70 75 80
 Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
 85 90 95
 Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
 100 105 110
 Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Arg Ser
 115 120 125
 Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
 130 135 140
 Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
 145 150 155 160
 Lys Ser Ile Tyr Asp Ser Ser Gly Lys Ser Ser Lys Ile Ala Ile Ser

Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp
210 215 220

Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys
225 230 235 240

Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val
245 250 255

Ile

0210: 17

0211: 2343

0212: DNA

0213: Mus musculus

0210:

0211: CDS

0222: (131)..(990)

0400: 17

aggagctctg aggtggggccc taaaatccag cgctcccccag agaaaagcct tgcagagccc 60

tactccgggc cccagagccc agcaggctgc tgcgcgcgcca gggggcactg tgtgagagccc 120

ctatcttgga caccgggggc cccctccccc ggcccaggcg ggaggggggc gacggggggcc 180

atg ggg ggc caa ggc cga aag gag agt ttg tcc gaa tcc cga gat ttg 228
Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
1 5 10 15

gac ggc tcc tat gac cag ctt acg ggc cac cct cca ggg ccc agt aaa 276
Arg Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
20 25 30

aaa gcc ctg aag cag cgt ttc ctc aag ctg ctg ccg tgc tgc ggg ccc 324
Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
35 40 45

caa gcc ctg ccc tca gtc agt gaa aca tta gtt gcc cca gcc tcc ctt 372
Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro Ala Ser Leu
50 55 60

agg cca caa aga gcc cgc ccg ctg gac cca gac agc gtg gag gat gag 420
Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val Glu Asp Glu
65 70 75 80

ttt gaa cta tcc acg ctg tcc cac cag cct tat agt cta caa caa ctc 468
Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu
85 90 95

0210: 17
0211: 2343
0212: DNA
0213: Mus musculus

aag aaa att tat tct cag ttc ttt ccc caa aga gac tcc agc aac tac 612
 Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr
 130 135 140

ggt aat ttt ctc ttc aat gcc ttt gac acc aac cat gat ggc tct gtc 660
 Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val
 145 150 155 160

agt ttt gag gac ttt gtg gct ggt ttg tca gtg att ctt agg gga acc 708
 Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr
 165 170 175

aia gat gat aga ctg aac tgg gct ttc aac tta tat gac ctc aac aag 756
 Ile Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys
 180 185 190

gat ggc tgt atc acc aag gag gaa atg ctc gac atc atg aag tcc atc 804
 Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile
 195 200 205

tat gac atg atg ggc aag tac acc tac cct gcc ctc cgg gag gag gcc 852
 Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala
 210 215 220

cng agg gaa cac gtg gag agc ttc ttc cag aag atg gac aga aac aag 900
 Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys
 225 230 235 240

gac gcc gtg gtg acc att gag gaa ttc att gag tct tgt caa cag gac 948
 Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp
 245 250 255

gag aac atc atg agg tcc atg caa ctc ttt gat aat gtc atc 990
 Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 260 265 270

tagctcccca gggagagggg ttagtggtgc ccagggtaac catgctgtag ccttagtcca 1050

ggcacaaacta accctctctt ccccggtctt gtctcctcc tacctgtacc ctgggggctg 1110

tagggattca acatcctggc gcttcagtag tccagatccc tgagctaaat ggcgagagta 1170

ggaagctaa ctctttaga gctggttgg ggggacaa ctctttaga ggcgagagta 1230

tccacctt tagactgat accagctat gaggta cc ctctttaga ggcgagagta 1290

agtggttctc tgcctccca gccactcta gagaccaca ctagaaggga atatctctg 1350

ctatggtgtt tccccatcc ctgacccgag atttctctc taagactccc ttctcagaga 1410

atggttctt gctctttag ctgagggg ctctctgct agctttaga ggcgagagta 1470

ttaggatcca gatgtccggg ccatcctctga aactctccc tctctcttgc tctatagggtg 1770
 ggagtgggtg gagggggaag atgagtgagc cgtgtctctg gatgatgct gtcaagggtcc 1830
 aactaacct cgggtctga agcgttctg gtgacctgt ttgattctcc atgacctctg 1890
 tctagatgta gaggtgtgga gtgagtctag tggcagcctt aggggaatgg gaagaacgag 1950
 ggggcactc cactgaacc cagtgtgggg gcacccattc gaatctttgc ctggtctccc 2010
 caatgacct aggtctctt agggctccca ccccaactct ttagtctacc cagagatgct 2070
 cagagctca cctagagggg agggaccata ggtccaggt ccaactgtc atcagcatcc 2130
 ggcattctg ctgtctgcta ttaataaac tcttctgtct cagcgcccc tcccaagtc 2190
 ggcagggtct gaggggaagg ccccaacttt cccgctctct gtcagacatt gttgactgct 2250
 ttgcatcttg ggtctctcta cctatatttt gtataataag aagacacca gatccaataa 2310
 aacacatggc tctgcacaaa aaaaaaaaaa aaa 2343

-C10- 18
 -C11- 270
 -C12- PRT
 -C13- Mus musculus

-C10- 18
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Gln Ser Arg Asp Leu
 1 5 10 15
 Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
 20 25 30
 Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro Ala Ser Leu
 50 55 60
 Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val Glu Asp Glu
 65 70 75 80
 Phe Gln Leu Ser Thr Val Cys His Arg Pro Gln Gly Leu Gln Gln Leu
 85 90 95
 Gln Gln Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg
 100 105 110
 Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asp Ile
 115 120 125
 -C11- 270
 -C12- PRT
 -C13- Mus musculus
 Met Phe Ser Arg Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr

Ile Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys
180 185 190

Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile
195 200 205

Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala
210 215 220

Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys
225 230 235 240

Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp
245 250 255

Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
260 265 270

0110: 19
0111: 1955
0112: DNA
0113: Homo sapiens

0120:
0121: CDS
0122: (207)..(962)

0400: 19
ctacactgct gactagtgtt cctctctctg ctccaggacc tccgggtaga cctcagacac 60
cgggccatt cccagactca gctcagccc ggactccccc agccccgaca gcacagttagg 120
cggccagggg gggcgtgtg agggccat cccggccacc cggcgcctcc tcccagggc 180
cggcggggag cgggggcgcg ggggac atg cgg ggc cag ggc cgc aag gag agt 233
Met Arg Gly Gln Gly Arg Lys Glu Ser
1 5
ttg tcc gat tcc cga gac ctg gac ggc tcc tac gac cag ctg acg ggc 281
Leu Ser Asp Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly
10 15 20 25
atg gta gta gta ctc act gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa 334
His Pro Pro Gly Pro Thr Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys
30 35 40
ctg ctg cag tgc tgc ggg ccc gaa gac ctg ccc tca gtc agt gaa aat 377
Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Asn
45 50 55
agg gta gat gat gaa ttt gta ttt ttt ttt ttt ttt ttt ttt ttt ttt 430
Arg Val Asp Asp Gaa ttt gta ttt ttt ttt ttt ttt ttt ttt ttt ttt
435 440 445 450 455 460 465 470 475 480 485 490 495 500

0400: 19
ctacactgct gactagtgtt cctctctctg ctccaggacc tccgggtaga cctcagacac 60
cgggccatt cccagactca gctcagccc ggactccccc agccccgaca gcacagttagg 120
cggccagggg gggcgtgtg agggccat cccggccacc cggcgcctcc tcccagggc 180
cggcggggag cgggggcgcg ggggac atg cgg ggc cag ggc cgc aag gag agt 233
Met Arg Gly Gln Gly Arg Lys Glu Ser
1 5
ttg tcc gat tcc cga gac ctg gac ggc tcc tac gac cag ctg acg ggc 281
Leu Ser Asp Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly
10 15 20 25
atg gta gta gta ctc act gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa 334
His Pro Pro Gly Pro Thr Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys
30 35 40
ctg ctg cag tgc tgc ggg ccc gaa gac ctg ccc tca gtc agt gaa aat 377
Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Asn
45 50 55
agg gta gat gat gaa ttt gta ttt ttt ttt ttt ttt ttt ttt ttt ttt 430
Arg Val Asp Asp Gaa ttt gta ttt ttt ttt ttt ttt ttt ttt ttt ttt
435 440 445 450 455 460 465 470 475 480 485 490 495 500

0400: 19
ctacactgct gactagtgtt cctctctctg ctccaggacc tccgggtaga cctcagacac 60
cgggccatt cccagactca gctcagccc ggactccccc agccccgaca gcacagttagg 120
cggccagggg gggcgtgtg agggccat cccggccacc cggcgcctcc tcccagggc 180
cggcggggag cgggggcgcg ggggac atg cgg ggc cag ggc cgc aag gag agt 233
Met Arg Gly Gln Gly Arg Lys Glu Ser
1 5
ttg tcc gat tcc cga gac ctg gac ggc tcc tac gac cag ctg acg ggc 281
Leu Ser Asp Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly
10 15 20 25
atg gta gta gta ctc act gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa 334
His Pro Pro Gly Pro Thr Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys
30 35 40
ctg ctg cag tgc tgc ggg ccc gaa gac ctg ccc tca gtc agt gaa aat 377
Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Asn
45 50 55
agg gta gat gat gaa ttt gta ttt ttt ttt ttt ttt ttt ttt ttt ttt 430
Arg Val Asp Asp Gaa ttt gta ttt ttt ttt ttt ttt ttt ttt ttt ttt
435 440 445 450 455 460 465 470 475 480 485 490 495 500

Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val
 90 95 100 105

aat gag gag aac ttc aag cag att tac tcc sag ttc ttt cct caa gga 569
 Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly
 110 115 120

gac tcc agc acc tat gcc act ttt ctc ttc aat gcc ttt gag acc aac 617
 Asp Ser Ser Thr Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn
 125 130 135

cat gat ggc tgg gtc agt ttt gag gac ttt ggg gct ggt ttg tcc gtg 665
 His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val
 140 145 150

att att cgg gga act gta gat gac agg ctt aat tgg gcc ttc aac ctg 713
 Ile Leu Arg Gly Thr Val Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu
 155 160 165

tat gac ctt aac aag gac ggc tgc atc acc aag gac gaa atg att gac 761
 Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp
 170 175 180 185

atc atg aag tcc atc tat gac atg atg gcc aag tac aag tac cct gca 809
 Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala
 190 195 200

ctc cgg gag gag gcc cca agg gaa cac gtg gag agc ttc ttc cag aag 857
 Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys
 205 210 215

atg gac aga aac aag gat ggt gtg gtg acc att gag gaa ttc att gag 905
 Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu
 220 225 230

tct tgt caa aag gat gag aac atc atg agg tcc atg bag ctc ttt gac 953
 Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp
 235 240 245

aat gtc atc tagccccag gagagggggt cagtgtttcc tggggggacc 1002
 Asn Val Ile
 250

atgtcttaac cctagctccag gaggacatca cactctctct ccaggtctca tctctatct 1067
 acgcctccct gggggct gga ggcctccaaag acctctctca ttcagctatc cactctctct 1127
 gagctgaag ggcagagag tgggcagagt gcattctggg ggggtgttccc aactccacc 1182
 agctctccac ccttctctgc ctgacaccca gtgttgagag tgcctctctc gtagggaattg 1242
 aggtctctct cctctctctc cctctctctc cctctctctc gagagatgct tctgtctatg 1302

agctccaaagt tccacagggtc tgcctaccaca ggccatcaaa atataagttt ccagggtttg 1602
 cagaagacct tgtctcccta gaaatgcccc agaaattttt cacaacttc ccggtatcca 1662
 tggagagacct ggggcccagat atctggctca tctctggcat tgccttctct ccttcttcc 1722
 tgcattgttt ggagggtggtt gtggtggggg aatgtggatg ggggatgtcc tggctgatgc 1782
 ctgcacaaaat ttatcccaac cctccttgcct tatcgtccct gttttgaggg ctatgacttg 1842
 agtttttgtt tccatgttc tctatagact tgggaccttc ctgaacttgg ggccatcac 1902
 tcccaacagt ggatgcctta gaagggagag ggaaggaggg aggcaggcat agc 1955

K210> 20
 K211> 252
 K212> PRT
 K213> Homo sapiens

K400> 20
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu
 1 5 10 15
 Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Thr Lys
 20 25 30
 Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Asp Asp Glu Phe Glu
 50 55 60
 Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
 65 70 75 80
 Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg Gly Phe
 85 90 95
 Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
 100 105 110
 Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
 115 120 125
 Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 130 135 140
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
 145 150 155 160
 Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
 165 170 175

K210> 20
 K211> 252
 K212> PRT
 K213> Homo sapiens

K400> 20
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu

210

215

220

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn
 125 230 235 240

Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 245 250

<210> 21

<211> 2300

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (214)..(969)

<400> 21

ctcatttget gcccaagggt cctgctcctg cccagggaat ctgaggttggg cccataaaac 60

cagcgtcttc taaagaaaag ccttgccagc cctactcc ggcccccac cccagcaggt 120

cctggtccg ccagggggcg ctgtgtgagc ggcctattct ggcacccgg cgcctctcc 180

ccaggccag gggggagcgg gggtccgggg gcc atg cgg ggc caa ggc aga aag 234
 Met Arg Gly Gln Gly Arg Lys
 1 5

gag agt ttg tcc gaa tcc cga gat ctg gac ggc tcc tat gac cag ctt 282
 Glu Ser Leu Ser Glu Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu
 10 15 20

acg ggc cac cct cca ggg ccc agt aaa aaa gcc ctg aag cag cgt ttc 330
 Thr Gly His Pro Pro Gly Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe
 25 30 35

ctc aag ctg ctg ccg tgc tgc ggg ccc caa gcc ctg ccc tca gtc agt 378
 Ser Lys Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser
 40 45 50 55

gaa aac agc gta gag gat gag ttt gaa tta tcc acg ggc tgt cac cga 426
 Glu Asn Ser Val Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg
 60 65 70

ctt tat ggt ctg gaa caa ctg cag gaa cag acc aat ttc gta ctt gta 474
 Pro Glu Gly Leu Thr Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg
 75 80 85

gag ctg cag gtc ctg tac cga gcc ttc aag aac gaa tgc ccc agt ggg 522
 Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
 90 95 100

<400> 21

gag agt ttg tcc gaa tcc cga gat ctg gac ggc tcc tat gac cag ctt 282
 Glu Ser Leu Ser Glu Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu
 10 15 20

acc aac cac gat ggc tct gtc agt ttt gag gac ttt gtg got ggt ttg 666
 Thr Asn His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu
 140 145 150

tgg gtg att ctt cgg ggg acc ata gat gat aga ctg agc tgg got ttc 714
 Ser Val Ile Leu Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe
 155 160 165

aac tta tat gac ctc aac aag gac ggc tgt atc aca aag gag gaa atg 762
 Asn Leu Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met
 170 175 180

ctt gac att atg aag tcc atc tat gac atg atg ggc aag tac aca tac 810
 Leu Asp Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
 185 190 195

cct gcc ctc cgg gag gag gcc cca aga gaa cac gtg gag agc ttc ttc 858
 Pro Ala Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe
 200 205 210 215

cag aag atg gac agg aac aag gac ggc gtg gtg acc atc gag gaa ttc 906
 Gln Lys Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe
 220 225 230

atc gag tct tgt caa cag gac gag aac atc atg agg tcc atg cag ctc 954
 Ile Glu Ser Cys Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu
 235 240 245

ttt gat aat gcc atc tagctcccca gggagagggg ttagtgtgtc ctagggtgac 1009
 Phe Asp Asn Val Ile
 250

caggtgttag tcttagtcca gacgaaccta acctctcttc tccaggcctg tctcatttt 1059
 acctgtaccc tgggggctgt agggattcaa tctctgggg cticagtagt ccagatccct 1129
 gagctaagtc acaaaagtag gcaagagtag gcaagctaaa tctgggggct tcccaacccc 1189
 cgacagctct caccctctct caactgatac ctagtgtgta ggacacccct ggtgtaggga 1249
 ccaagtgggt ctccaccttc tagtccact ctagaaacca cattagacag aaggtctctt 1309
 gotatgggtgc ttcccccata cctaattctct tagatttcc tcaagactcc ctctcagag 1369
 aacacccctct gtcctgttcc ccagcttctc tctgactc gctctcagc gctctcagc 1429
 caggtgttgc caggaagga gaaaagtctt ggcctccagc cagtgggttag gtcctaggaa 1489
 ttgggtggag tggaggccag aaagcctggg cagatgatga gagccacgct ggggtgtcac 1549
 tgcaggttcc ggggcctaca ggccttggtc accagactat gacttccag actttccaga 1609
 aggtccttag caatgtccca gaaattcagc gacattct gacttctc gacttctc gacttctc

aggggaatg; gaagaaccca atgtgggggc acacattag; atcttggc ggctccctac 1969
 aatgccttag ggctcccttag ggtaccggt cctctgttt agtctacca gagatgctcc 2029
 ttagctcacc tagagggtag ggaagggtag ctccaggtcc aacctctcca ggctcagcacc 2089
 ctgcctatgt gctgctctctc attaacaacac ctgcttgtct cctctctgct cctctctcag 2149
 tcagccaggg tctgagggga agggctctcc gtttccctat cctcagaca tgggtgactg 2209
 ctttgcattt tctgctctctc tatctatttt gtaaaataag acatcagatc caataaacca 2269
 cacgctatg caaaaaaaaa aaaaaaaaaa a 2300

<210> 22
 <211> 252
 <212> PRT
 <213> Rattus sp.

<400> 22
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
 1 5 10 15
 Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
 20 25 30
 Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Glu Asp Glu Phe Glu
 50 55 60
 Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
 65 70 75 80
 Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe
 85 90 95
 Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
 100 105 110
 Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr Ala Thr
 115 120 125
 Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 130 135 140
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp
 145 150 155 160
 Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asn Leu Leu Leu Leu Leu
 165 170 175 180 185 190 195 200

Met Met Lys Lys Lys Lys Lys Lys Ala Leu Asn Ser Leu Ala Leu Arg
 205 210 215 220 225 230 235 240 245 250

Glu His Val Glu Ser Phe Phe Glu Lys Met Asp Arg Asn Lys Asp Gly
 210 215 220

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp Glu Asn
425 338 235 240

Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
245 250

```

#210: 23
#211: 1859
#212: DNA
#213: Homo sapiens

```

```

0220>
0221> CDS
0222> (207) .. (866)

```

```

04000: 23
ctacacagct gactagtgtt cactctctgt ctccaggacc tcggggtaga cctcagaccc 60
gggggcatt cccagactca gctcagccc ggacttcccc agccccgaca gcacagttagg 120
tcgcaggagg gggcctgtgt agcgccctat ccgggcacac cggcgccccc tcccaggccc 180
ggggggggag cggggggcgc ggggcc atg cgg ggc cag ggc cgc aag gag agt 233
Met Arg Gly Gln Gly Arg Lys Glu Ser
1 5

```

ttg tcc gat tcc cga gac ctg gac ggc tcc tac gac cag ctg acg gac 251
 leu ser asp ser arg asp leu asp gly ser tyr asp gln leu thr asp
 10 15 20 25

agc ggc gac gat gaa ttt gaa ttg tcc acc gtg tgt cac cgg gcc gag 329
 Ser Val Asp Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu
 30 35 40

ggt ctg gag cag ctg cag gag caa acc aaa ttc acg cgc aag gag ttg 377
Gly Leu Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Lys Glu Leu
45 50 55

Cag gtc ctg tac cgg ggc ttc aag aac gaa tgt ccc agc gga att gtc 421
 Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val
 60 60 60

cat gag gag aag ttc aag cag att tac tcc sag ttc ttt tct caa gga 473
 Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly
 75 80 85

gag tgc agc aac tat ggc act ttt cta tta aat gaa ttt taa aat aac 501
 Asp Ser Ser Thr Tyr Ala Thr Glu Leu Phe Asn Ala Phe Asp Thr Asn
 95 100 105

Val, Met, Ile, Leu, Arg, Thr, Lys, Ile, Val, Thr, Asp, Glu, Ile, Ile, Ile, Thr, Lys, Val, Lys, Arg, Thr, Val, Asp, Asp, Asp, Leu, Asp, Tyr, Ala, Val, Asp, Lys

tat gac ctt aac aag gac ggc tgc atc acc aag gag gaa atg ctt gac 665
 Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp
 140 145 150

atc atg aag tcc atc tat gac atg atg ggc aag tac acg tac cct gca 713
 Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala
 155 160 165

ctc cgg gag gag gcc cca agg gaa cac gtg gag agc ttc ttc gag aag 761
 Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys
 170 175 180 185

atg gac aga aac aag gat ggt gtg gtg acc att gag gaa ttc att gag 809
 Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu
 190 195 200

tct tgt caa aag gat gag aac atc atg agg tcc atg gag ctc ttt gac 857
 Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp
 205 210 215

aat gtc atc tagccccag gagagggggg cagtgtttcc tgggggggacc 906
 Asn Val Ile
 220

atgctctaac cctagtcacg ggggacctca cccctctctt ccaggtcta tctcctct 966
 acgctccct ggggggtgga gggatccaag agcttgggga ttcagtagtc cagatctctg 1026
 gagctgaagg ggcacagagag tgggcagagt gcatctcggg ggtgtttccc aactccacc 1086
 agctctcacc ccttctctgc ctgacaccca gtgttgagag tgcctctct gtagggaattg 1146
 agcgtttccc cactctctac cctactctag aaacacacta gagcgatgtc tctgctatg 1206
 gtgcttccc cctccttgac ctacataaaca tttcccttaa gactccctc tcagagagaa 1266
 tgcctcatto ttggcaactgg ctggctcttc agaccagcca ttgagagccc tgtgggaggg 1326
 ggacaagaat gtatagggag aaatcttggg cctgagtcac tggataggtc ctaggaggtg 1386
 ggtgggggtt agaatagaag ggcttgaca gattatgatt gctcaggeat accaggttat 1446
 agctcvaagt tccacaggtc tctacacaca ggcctcaca atataagtt caggtttt 1506
 cagaagact tctctctta gaaatgcac aaaaatttt cacacatc tgggtttt 1566
 tggagagcct ggggcacgat atctggtca tctctggcat tcttctct ccttctct 1626
 tgcctgtgtt ggtggtggtt gtggtggggg aatgtggat ggggatgtc tgggtgag 1686
 ctgcacaaa tctacacac cttctctgt tctctctt gtcttgagg ctatgact 1746

<013> Homo sapiens

44007 24

Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu
1 5 10 15

Asp Gly Ser Tyr Asp Gln Leu Thr Asp Ser Val Asp Asp Glu Phe Glu
20 25 30

Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
35 40 45

Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg Gly Phe
50 55 60

Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
65 70 75 80

Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
85 90 95

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
100 105 110

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
115 120 125

Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
130 135 140

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
145 150 155 160

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
165 170 175

Glu His Val Glu Ser Phe Phe Glu Lys Met Asp Arg Asn Lys Asp Gly
180 185 190

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn
195 200 205

Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
216 215 220

• **•**

2110 2191

<212> DNA

<213> Simian sp.

• 222 •

4217 CDS

1. *Staphylococcus aureus* 2. *Staphylococcus epidermidis* 3. *Staphylococcus saprophyticus* 4. *Staphylococcus sciuri* 5. *Staphylococcus carnosus* 6. *Staphylococcus hyicus* 7. *Staphylococcus epidermidis* 8. *Staphylococcus aureus* 9. *Staphylococcus aureus* 10. *Staphylococcus aureus* 11. *Staphylococcus aureus* 12. *Staphylococcus aureus* 13. *Staphylococcus aureus* 14. *Staphylococcus aureus* 15. *Staphylococcus aureus* 16. *Staphylococcus aureus* 17. *Staphylococcus aureus* 18. *Staphylococcus aureus* 19. *Staphylococcus aureus* 20. *Staphylococcus aureus* 21. *Staphylococcus aureus* 22. *Staphylococcus aureus* 23. *Staphylococcus aureus* 24. *Staphylococcus aureus* 25. *Staphylococcus aureus* 26. *Staphylococcus aureus* 27. *Staphylococcus aureus* 28. *Staphylococcus aureus* 29. *Staphylococcus aureus* 30. *Staphylococcus aureus* 31. *Staphylococcus aureus* 32. *Staphylococcus aureus* 33. *Staphylococcus aureus* 34. *Staphylococcus aureus* 35. *Staphylococcus aureus* 36. *Staphylococcus aureus* 37. *Staphylococcus aureus* 38. *Staphylococcus aureus* 39. *Staphylococcus aureus* 40. *Staphylococcus aureus* 41. *Staphylococcus aureus* 42. *Staphylococcus aureus* 43. *Staphylococcus aureus* 44. *Staphylococcus aureus* 45. *Staphylococcus aureus* 46. *Staphylococcus aureus* 47. *Staphylococcus aureus* 48. *Staphylococcus aureus* 49. *Staphylococcus aureus* 50. *Staphylococcus aureus* 51. *Staphylococcus aureus* 52. *Staphylococcus aureus* 53. *Staphylococcus aureus* 54. *Staphylococcus aureus* 55. *Staphylococcus aureus* 56. *Staphylococcus aureus* 57. *Staphylococcus aureus* 58. *Staphylococcus aureus* 59. *Staphylococcus aureus* 60. *Staphylococcus aureus* 61. *Staphylococcus aureus* 62. *Staphylococcus aureus* 63. *Staphylococcus aureus* 64. *Staphylococcus aureus* 65. *Staphylococcus aureus* 66. *Staphylococcus aureus* 67. *Staphylococcus aureus* 68. *Staphylococcus aureus* 69. *Staphylococcus aureus* 70. *Staphylococcus aureus* 71. *Staphylococcus aureus* 72. *Staphylococcus aureus* 73. *Staphylococcus aureus* 74. *Staphylococcus aureus* 75. *Staphylococcus aureus* 76. *Staphylococcus aureus* 77. *Staphylococcus aureus* 78. *Staphylococcus aureus* 79. *Staphylococcus aureus* 80. *Staphylococcus aureus* 81. *Staphylococcus aureus* 82. *Staphylococcus aureus* 83. *Staphylococcus aureus* 84. *Staphylococcus aureus* 85. *Staphylococcus aureus* 86. *Staphylococcus aureus* 87. *Staphylococcus aureus* 88. *Staphylococcus aureus* 89. *Staphylococcus aureus* 90. *Staphylococcus aureus* 91. *Staphylococcus aureus* 92. *Staphylococcus aureus* 93. *Staphylococcus aureus* 94. *Staphylococcus aureus* 95. *Staphylococcus aureus* 96. *Staphylococcus aureus* 97. *Staphylococcus aureus* 98. *Staphylococcus aureus* 99. *Staphylococcus aureus* 100. *Staphylococcus aureus*

Met	Arg	Gly	Gln	Gly	Arg	Lys	Glu	Ser	Leu	Ser	Asp	Ser	
1				5								10	
cga gac ctg gac gga tcc tac gac cag ctc acg gac agc gtg gag gat	219												
Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Asp Ser Val Glu Asp													
15 20 25													
gaa ttt gaa ttg tcc acc gtg tgt cac cgg cct gag ggt ctg gag cag	267												
Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln													
30 35 40 45													
ctg cag gag caa acc aaa ttc aag cgc aag gag ttg cag gtc ctg tac	315												
Leu Gln Glu Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr													
50 55 60													
cgg ggc ttc aag aac gaa tgt ccg agc gga att gtc aat gag gag aac	363												
Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn													
65 70 75													
ttc aag caa att tac tcc cac ttc ttt cct caa gga gac tcc agc acc	411												
Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr													
80 85 90													
tat gcc act ttt ctc ttc aat gcc ttt gac acc aac cat gat ggc tgg	459												
Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser													
95 100 105													
gtc agt ttt gag gac ttt gtg ggt ggt ttg tcc gtg att ctt cgg gga	507												
Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly													
110 115 120 125													
act gta gat gac agg ctt aat tgg gcc ttc aac ttg tat gac ctc aac	555												
Thr Val Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn													
130 135 140													
aag gac ggc tgc atc acc aag gag gaa atg ctt gac atc atg aag tcc	603												
Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser													
145 150 155													
atc tat gac atg atg ggc aag tac aca tac cct gca ctc cgg gag gag	651												
Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu													
160 165 170													
gac cca agg gaa cat gtg gag aac ttc ttc cag aag atg gac gaa aac	699												
Ala Pro Arg Glu His Val Thr Asn Phe Phe Gln Lys Met Asp Arg Asn													
175 180 185													
aag gat ggc gtg gtg acc att gag gaa ttc att gag tct tgt caa aag	747												
Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys													
190 195 200 205													
gat gag aac atc atg agg tcc atg cag ctc ttt gac aat gtc atc	792												
Asp Glu Asn Ile Met Arg Ser Met Thr Thr Phe Thr Thr Thr Thr													

tgggagagagt	gaatattggg	gggtgttcc	aaattccacc	agatttcacc	agtttcctgc	1032
ctgacaacaa	gtgttgagag	tgcctctct	gtaggaaatg	agtgggttcc	caactctac	1092
ccccattcta	gaaanacact	agacagatgt	ctctgtctat	ggtgttccc	ccatccatga	1152
cttcataaac	atttccctta	aaaatccctt	ctcagagaga	atgtctcatt	cttgggactg	1212
gctggcttct	cagaccagcc	tttgagagcc	ctgtgggagg	gggacaagaa	tgtatagggg	1272
agaaatcttg	ggcttgagtc	aatggatagg	tcctaggagg	tgggtggggg	tgagaataga	1332
aaggcctgga	cacaatgtga	ttgttcaggc	ataccaagtt	atagctccaa	gttcacacgg	1392
tctgtctaca	caggccatca	aaatataagt	ttccagggtt	tgcagaagac	cttgtctctc	1452
tggaaatgcc	ccagatattt	cccataccct	ctctgatctc	catgggagagc	ctggggctag	1512
atatctggca	tatccctggc	attgcttctc	ctccttccct	ctgtcatgtg	ttgggtgggtg	1572
ttgtggcagg	ggaatgtgga	taggagatgt	ctcggccagat	gcctggccaaa	gtttcatccc	1632
acctccctg	ctcatcgccc	ctgttttgag	ggtgtgtgact	tgagtctctg	tttcccatgt	1692
tctctataga	cttgggaact	tcctgaaact	ggggcctatc	actcccacaa	gtggatgcct	1752
tagaaggggag	agggaaggag	ggagggcaggc	atagcatctg	aaaccagtgt	gggggcattc	1812
actaggatct	tcaatcaacc	ggggctctcc	ccaaaccccc	agataacctc	ctcagttccc	1872
tagagtctcc	tcttgcctta	ctcaatctac	ccagagatgc	cccttagcac	actcagaggy	1932
cagggacat	aggaccagg	ttccaaacccc	attgtcagca	ccccagccat	gctgccatcc	1992
cttagcacac	ctgtctgccc	cattcagctt	acctcccacg	tcagccagaa	tctgagggga	2052
gggccccacg	agagcccct	tcctccatcag	aagaactgtg	actgcttgc	attttgggt	2112
cttctatata	ttttgtaaaa	taagaactat	accagatcta	ataaaacaca	atggctatgc	2172
aaaaaaaaaa	aaaaaaaaaa					2191

<210> 36
<211> *Stenocentrus*
<212> 1KT
<213> Similan sp.

<400> 26
Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu
1 5 10 15

Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
65 70 75 80

Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
85 90 95

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
100 105 110

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
115 120 125

Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
130 135 140

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
145 150 155 160

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
165 170 175

Glu His Val Glu Asn Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
180 185 190

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn
195 200 205

Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
210 215 220

00100: 27

00110: 2057

00120: DNA

00130: Simian sp.

00200:

00210: CDS

00220: (208)..(963)

04000: 27

tgtctcccaaa ggtctcttgt cctgccccag gaactctgagg tgggccttaa aaccacagcc 60

tctctaaaga aaagctcttg cagccctctc tctcgccttc caacacagc agtcctctc 120

gagccacagg ggcctctctc cagcctctta tctctctc aggggcctc ctctcaggg 180

ccaggcggga gggggggccc gggggccc atg cgg ggc caa ggc aga aag gag agt 240

Met Arg Gly Gln Gly Arg Lys Glu Ser

1

5

atg ttc caa tctcaga gat atg gat ggc ttc tat gac cag ctt aag ggc 300

Leu Ser Glu Ser Arg Asn Leu Ser Glu Gln Thr Thr Thr Thr

Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Asn
 45 53 55
 agc gta gag gat gag ttt gaa tta tcc acg gtg tgt cac cga cct gag 426
 Ser Val Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu
 60 65 70
 ggc ctg gaa caa ctg cag gaa cag acc aag ttc aca cgc aga gag ctg 474
 Gly Leu Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu
 75 80 85
 cag gtc ctg tac cga ggc ttc aag aac gaa tgc ccc agt ggg att gtc 522
 Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val
 90 95 100 105
 aac gag gag aac ttc aag cag att tat tct cag ttc ttc ccc caa gga 570
 Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly
 110 115 120
 gac tcc agc aac tat ggt act ttt ctg ttc aat gcc ttt gac acc aac 618
 Asp Ser Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn
 125 130 135
 cac gat ggc tct gtc agt ttt gag gac ttt gtg gct ggt ttg tgg gtg 666
 His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val
 140 145 150
 att ctg cgg ggg aac ata gat gat aga ctg agc tgg gct ttc aac tta 714
 Ile Leu Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu
 155 160 165
 tat gac ctg aac aag gac ggc tgt atc aca aag gag gaa atg ctg gac 762
 Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp
 170 175 180 185
 att atg aag tcc atc tat gac atg atg ggc aag tac aca tac cct gcc 810
 Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala
 190 195 200
 ctg cgg gag gag gcc cca aga gaa cac gtg gag agc ttc ttc cag aag 858
 Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys
 205 210 215
 atg gac agg aac aag gac agt ctg gtg aac atc gag gaa ttc atc gag 906
 Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Ile Ile Glu
 220 225 230
 tct tgt caa cag gac gag aac atc atg agg tcc atg cag ctg tca ccc 954
 Ser Cys Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu Ser Pro
 235 240 245
 att ctg aac tgaatcag tgcaggagc aacccaggtc tagggaccaa 1008
 Leu Leu Asn

tggggacaaag aaagcagaaaa agtcttgagg ccagagccagt ggcttaggtcc taggaattgg 1243
 ctggagtggg ggcacagaaag cctgggcaga tgatgagaga ccagctgggc tgcacactgca 1303
 ggcttcggggg cctacagccc tgggtcagca gactatgagt tccagactt tccagaaggt 1363
 ccttagcaat gtccagaaaa ttcacccgtac actttctcagt gtcttaggag ggcccgggat 1423
 ccagatgtct ggcttcaccc tgaatccctt ccttccttct tgcctgtatg gtgggagtgg 1483
 tggccagggg aagatgagtg gtgtcccgga tgatgcctgt caaggtccca cctccctcc 1543
 ggctgttctc atgacagctg ttctgttctc catgacccct atctagatgt agaggcatgg 1603
 agtgagttag ggatttcctg aacttgagtt taccacctc ccttagtggc tgccttaggg 1663
 gaatgggaag aaccacagtg gggggcacc attagaatct ttgcccgggt cctcacaatg 1723
 ccttagggtc ccttagggta ccgctccct ctgtttagtc taccagaga tgcctctgag 1783
 ctcacctaga ggttagggac ggtaggtcc aggtccacc tctccaggtc agcacctgc 1843
 catgtgtgtg ctctcatta acaaacctgc tctctctc ctgcgcctt tctcagtcag 1903
 ccagcgtctg aggggaaggg cctcccgttt ccccatccgt cagacatggt tgaactgctt 1963
 gcattttggg ctctctctatc tattttgtaa aataagacat cagatccaat aaaacacacg 2023
 gctatgcaca aaaaaaaaaa aaaaaaaaaa aaaa 2057

(210): 28

(211): 282

(212): PRT

(213): Simian sp.

(400): 28

Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
 1 5 10 15

Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
 20 25 30

Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45

Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Glu Asp Gln Phe Glu
 50 55 60

Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
 65 70 75 80

Gln Thr Lys Phe Thr Arg Arg Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr

Leu Lys Thr Gln Leu Leu Leu Leu Gln Lys Arg Ser Ser Asn Tyr Ala Thr
 85 90 95 100 105 110 115 120 125 130 135 140 145 150

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 135 135 140
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp
 145 150 155 160
 Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
 165 170 175
 Lys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
 180 185 190
 Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
 195 200 205
 Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
 210 215 220
 Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp Glu Asn
 225 230 235 240
 Ile Met Arg Ser Met Gln Leu Ser Pro Leu Leu Asn
 245 250

00100: 29
 00110: 1904
 00120: DNA
 00130: Rattus sp.

00200:
 00210: CDS
 00220: (1)..(675)

00300: 29
 atg aac caa tgc cct cgc agg tgc cgg agc cgg ttg ggg cag gca gct 48
 Met Asn His Cys Pro Arg Arg Cys Arg Ser Pro Leu Gly Gln Ala Ala
 1 5 10 15
 cga tct ctc tac cag ttg gta act ggg tgg ctg tgg cca gac agc gta 96
 Arg Ser Leu Tyr Gln Leu Val Thr Gly Ser Leu Ser Pro Asp Ser Val
 20 25 30
 gag gat gat tat aaa cta tcc aag gta tat cac aga cct gat ggc ctg 144
 Glu Asp Glu Phe Glu Leu Ser Thr Val Tyr His Arg Pro Glu Gly Leu
 35 40 45
 gaa caa ctc cag gaa cag acc aag ttc aca cgc aga gag ctg cag gtc 192
 Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
 50 55 60
 atg tac cga ggt ttc aag aac gaa tgc cca agt ggg att gtc aac gag 240
 Met Tyr Asp Gly Thr Leu Thr Ser Pro Thr Thr Thr Thr Thr Thr Thr

100										105										110									
ggc	tct	gtc	agt	ttt	gag	gac	ttt	gtg	gct	ggc	ttg	tgc	gtg	att	ctt	854													
Gly	Ser	Val	Ser	Phe	Glu	Asp	Phe	Val	Ala	Gly	Leu	Ser	Val	Ile	Leu														
115					120					125																			
egg	ggg	acc	ata	gat	gat	aga	ctg	agg	tgg	gct	ttc	aac	tta	tat	gac	432													
Arg	Gly	Thr	Ile	Asp	Asp	Arg	Leu	Ser	Trp	Ala	Phe	Asn	Leu	Tyr	Asp														
130					135					140																			
ctc	aac	aag	gac	ggc	tgt	atc	aca	aag	gag	gaa	atg	ctt	gac	att	atg	480													
Leu	Asn	Lys	Asp	Gly	Cys	Ile	Thr	Lys	Glu	Glu	Met	Leu	Asp	Ile	Met														
145					150					155					160														
aag	tcg	atc	tat	gac	atg	atg	ggc	aag	tac	aca	tac	cct	gac	ctc	egg	528													
Lys	Ser	Ile	Tyr	Asp	Met	Met	Gly	Lys	Tyr	Thr	Tyr	Pro	Ala	Leu	Arg														
165					170					175																			
gag	gag	gac	cca	aga	gaa	cac	gtg	gag	agg	ttc	ttc	cag	aag	atg	gac	576													
Glu	Glu	Ala	Pro	Arg	Glu	His	Val	Glu	Ser	Phe	Phe	Gln	Lys	Met	Asp														
180					185					190																			
agg	aac	aag	gac	ggc	gtg	gtg	acc	atc	gag	gaa	ttc	atc	gag	tct	tgt	624													
Arg	Asn	Lys	Asp	Gly	Val	Val	Thr	Ile	Glu	Glu	Phe	Ile	Glu	Ser	Cys														
195					200					205																			
caa	cag	gac	gag	aac	atc	atg	agg	tcg	atg	cag	ctc	ttc	gat	aat	gtc	672													
Gln	Gln	Asp	Glu	Asn	Ile	Met	Arg	Ser	Met	Gln	Leu	Phe	Asp	Asn	Val														
210					215					220																			
atc tagctcccca gggagagggg ttagtgtgtc ctagggtgac cagggtgtag 725																													
Ile 225																													
tcttagtcca gaagaaacta acctctcttc tccaggcctg tcttcattct acctgtacc 785																													
tgggggctgt agggattcaa tatcctgggg ctccagtagt ccagatccct gagctaagtc 845																													
acaaaagtag gcaagagtag gcaagctaaa tctgggggct tcccaacccc cgacagctct 905																													
caccctctct caactgatac ctagtgtgtg ggacacccct ggtgtaggga ccaagtgggt 965																													
ctccaccttc tagtccact ctapaaaca cattagacag aagttctct gctatggtg 1025																													
tttccctctc ctactctt tgggttttc tcttctctc ctccagag aagattctt 1085																													
gtccatgtcc ccagctggtt tctcagctta gcttttgagg gacctgtggg gaggggggga 1145																													
caagaaagca gaaaagtctt ggcccagaga tagtggttag gtctaggaa ttgggtggag 1205																													
tggatctag aaatttggt ttgtgtatc ggggttagt ttgtgtcac tttggttt 1265																													
ttttttttt tttttttt tttttttt tttttttt tttttttt tttttttt 1325																													

ttcttcacaaa tgcctatagg tccctatagg taaccgctcc ctatgttttag tctacccaga 1625
 gatgtctctg agctcaccct gagggtaggg acggtaggct ccaggtccaa cctctccagg 1685
 ccagtcacct gcctatgtgc tgcctctcat taacaaacct gcttgcctcc tctgagcccc 1745
 ttcttcagtc agccaggggtc tgaggggaag ggctccctgt tcccccctcc gtcagacatg 1805
 gttgactgct ttgcattttg ggcctcttcta tctattttgt aaaataagac atcagatcca 1865
 ataaacaca cggctatgca caaaaaaaaa aaaaaaaaaa 1904

4210 - 30
 4211 - 225
 4212 - PRT
 4213 - Rattus sp.

4400 - 30
 Met Asn His Cys Pro Arg Arg Cys Arg Ser Pro Leu Gly Gln Ala Ala
 1 5 10 15
 Arg Ser Leu Tyr Gln Leu Val Thr Gly Ser Leu Ser Pro Asp Ser Val
 20 25 30
 Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
 35 40 45
 Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
 50 55 60
 Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
 65 70 75 80
 Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser
 85 90 95
 Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
 100 105 110
 Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
 115 120 125
 Arg Gly Thr Ile Asp Asp Arg Leu Ser Tyr Ala Phe Asn Leu Tyr Asp
 130 135 140
 Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met
 145 150 155 160
 Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg
 165 170 175

His His Arg His Asn Ile Met Asn Ser Met His Ser His Ser His Thr

Ile
225

<210> 31
<211> 2841
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(768)

<100> 31
atg cag ccg gct aag gaa gtg aca aag gag tgg gac ggc agc ctc ctg 48
Met Gln Pro Ala Lys Glu Val Thr Lys Ala Ser Asp Gly Ser Leu Leu
1 5 10 15
ggg gac ctc ggg cac aca cca ctt agc aag aag gag ggt atc aag tgg 96
Gly Asp Leu Gly His Thr Pro Leu Ser Lys Lys Glu Gly Ile Lys Trp
20 25 30
cag agc ccg agc ctc agc cgc cag gct ttg atg aga tgc tgc ctg gtc 144
Gln Arg Pro Arg Leu Ser Arg Gln Ala Leu Met Arg Cys Cys Leu Val
35 40 45
aag tgg atc ctg tcc agc aca gcc cca cag ggc tca gat agc agc gac 192
Lys Trp Ile Leu Ser Ser Thr Ala Pro Gln Gly Ser Asp Ser Ser Asp
50 55 60
agt cag ctg gag ctg tcc aag gtg cgc cac cag cca gag ggg ctg gac 240
Ser Gln Leu Glu Leu Ser Thr Val Arg His Gln Pro Gln Gly Leu Asp
65 70 75 80
cag ctg cag gcc cag acc aag ttc acc aag aag gag ctg cag tct ctc 288
Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu
85 90 95
tac agg ggc ttt aag aat gag tgt ccc acg ggc ctg gtg gac gaa gac 336
Tyr Arg Gly Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp
100 105 110
acc ttc aaa ctc att tac gcc cag ttc ttc cct cag gaa gat gac aac 384
Thr Phe Lys Leu Ile Tyr Ala Gln Phe Phe Pro Gln Gly Asp Ala Thr
115 120 125
acc tat gca cac ttc ctc ttc aac gcc ttt gat gcc gac ggg aac ggg 432
Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly
130 135 140
acc ttc cca ttt gag gac ttc ggg gtt ggc ctc tcc atc atg ctg agg 480
Ala Ile His Phe Gln Asn Phe Val Met Thr Thr Thr Thr Thr Thr Thr

180 185 190

100 atc tat gac atg atg ggc ggc cac acc tac ccc atc ctg cgg gag 624
 Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
 195 200 205

gac gag ccc gag gag cac ggc gag agg ttc ttc gag aaa atg gac cgg 672
 Asp Ala Pro Ala Glu His Val Glu Arg Phe Phe Glu Lys Met Asp Arg
 210 215 220

aac cag gat ggg gta gtg acc att gaa gag ttc ctg gag gcc tgt cag 720
 Asn Gln Asp Gly Val Val Thr Ile Glu Glu Phe Leu Glu Ala Cys Gln
 225 230 235 240

aag gat gag aac atc atg agc tcc atg cag ctg ttc gag aat gtc atc 768
 Lys Asp Glu Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
 245 250 255

taggacacgt ccaaaaggagt gcacggccac agccacctcc aaccccaaga aacctccatc 824
 ctgcacaggag cagcctccaa gaaactttta aaaaatagat ttgcacaaaag tgaacagatt 888
 gctacacaca cacacacaca cacacacaca cacacacaca cacagccatt catctgggct 948
 ggcagagggg acagagttca gggaggggct gactctggct aggggcagag tccaggagcc 1008
 ccagccagcc ctccccaggg cagcgaggcg aggcctgcctc tgggtgagtg gctgacagag 1068
 caggtctgca ggcacccagc tgcctgatgt caccacagaag ggcctcagat gccctgcag 1128
 ggcagggctc aatctccggt gtgacccac ctgctccgt tctccattct gcttcttgc 1188
 cacacagtg gcggccccc ggcctccctg gtctccctcc cgtagccact ctctgccac 1248
 tacctatgt cttagaaaag cctccacctc aggcacccag agggaccagc tgggggggag 1308
 gggggagagg gggtaatgga ggcbaagcct gcagctttct ggaaattctt cctgggggt 1368
 ccaggatcc cctgctaact cactgacctg gaagagctgg gtaccaggcc acccactgtg 1428
 ggcbaagcct gactgggtgag gggccactgg gccccattct cctccatgg caggaaggcg 1488
 ggggattca agttttagga tgggtctg gtgagacac tgaaggcact ctctgcagc 1548
 tccagcgt ccttgagc tctctgctt cgtgcttg ttagggga atctgggg 1608
 tgggctgta cacacccctc agcacagaat gtccctcca aggtctctt aggtccggg 1668
 aggaactgg ttcagagact ggcagccagg gacccgggg cagagctcag aggagtctgg 1728
 caagggctt cctccctc tctctgctt cctctcca tggccaca cctctctg 1788
 cccctctt cctccctt cctctctt cctctctt cctctctt cctctctt 1848

gaatgcaagc ccaaaagctgg agccaatggt gagggctgag agggctgtgg ctgggtgggc 2148
 agcagaaaac cccaggagga gagagatgct gctcccgctt gattggggcc tcaccagaa 2198
 ggaacccggt cccaggccgc atggcccttc caggaacatt cccacataat acattccatc 2268
 acagccagcc cagctccact cagggctggc cgggggagtc cccgtgtgac ccaagaggct 2328
 agccccaggg tgagccaggg cctcagagga aaggcagtat ggccgaggcc atggggggcc 2338
 ctgggcattc acacacagcc tggcctcccc tggggagctg catggaagcc tggctccagg 2448
 tccagggtg actggggggc tatgctccca ggagggcacc agctttccct ggctccagga 2508
 tcttttccct cccctccacc gctgccagc cctccagct ggtgtccatc tgcctctaac 2568
 gccaaaggct caggagagca tcaccaccac accctggcg gccctggct tggggccaga 2628
 ctggctgcac agcccaacca agaggggtct gctccccag ctgggaccca gacccggcgc 2688
 atgtctgcat ggcagaagcg tctccctgg ccacggcctg ggaggggtgt tctgtttctc 2748
 agcatccact aatattcagt cctgttatatt ttaataaaat aaacttgaca aaggaaaaaa 2808
 aaaaaaaaaa aattcctggc gcccggttct cca 2841

<210> 32

<211> 256

<212> PRT

<213> Homo sapiens

<400> 32

Met Gln Pro Ala Lys Glu Val Thr Lys Ala Ser Asp Gly Ser Leu Leu
 1 5 10 15

Gly Asp Leu Gly His Thr Pro Leu Ser Lys Lys Glu Gly Ile Lys Trp
 20 25 30

Gln Arg Pro Arg Leu Ser Arg Gln Ala Leu Met Arg Cys Cys Leu Val
 35 40 45

Lys Trp Ile Leu Ser Ser Thr Ala Pro Gln Gly Ser Asp Ser Ser Asp
 50 55 60

Ser Glu Leu Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp
 65 70 75 80

Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu
 85 90 95

Tyr Arg Gly Phe Thr Asp Gln Thr Lys Thr Thr Thr Thr Thr Thr Thr

Thr Tyr Ala His Thr Leu His Asp Ala Thr Arg Ala Arg Gly Arg Gly
 100 105 110 115

Lys Asp Glu Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
245 250 255

43000 - 33																	
tta	gag	gac	tta	gtg	gtt	ggg	ctc	tcc	atc	ctg	ctt	cga	ggg	acc	gtc	48	
Phe	Glu	Asp	Phe	Val	Val	Gly	Leu	Ser	Ile	Leu	Leu	Arg	Gly	Thr	Val		
1				5					10					15			
43000 - 34																	
cat	gag	aag	ctc	aag	tgg	gcc	ttc	aat	ctc	tac	gac	atc	aac	aag	gac	96	
His	Glu	Lys	Leu	Lys	Trp	Ala	Phe	Asn	Leu	Tyr	Asp	Ile	Asn	Lys	Asp		
			20					25					30				
43000 - 35																	
ggg	tac	atc	acc	aaa	cag	cag	atg	ctg	gcc	atc	atg	aag	tcc	atc	tac	144	
Gly	Tyr	Ile	Thr	Lys	Glu	Glu	Met	Leu	Ala	Ile	Met	Lys	Ser	Ile	Tyr		
		35					40					45					
43000 - 36																	
gtc	ata	gta	gag	gtc	gtc	gtc	gtc	gtc	atc	ctg	ggg	gag	gag	gta	gtc	147	
Asp	Met	Met	Gly	Arg	His	Thr	Tyr	Pro	Ile	Leu	Arg	Gln	Asp	Ala	Ile		
	50					55					60						
43000 - 37																	
ctg	gag	cat	gtg	cag	agg	ttc	ttc	cag	aaa	atg	gac	agg	aac	cag	gat	240	
Leu	Glu	His	Val	Glu	Arg	Phe	Phe	Gln	Lys	Met	Asp	Arg	Asn	Gln	Asp		
65					70					75				80			

[illegible]

gaagcctcta tgagaaacat tttctataa tatttgcaaa aagtg

442

<210> 34
 <211> 109
 <212> PRT
 <213> Rattus sp.

<400> 34
 Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg Gly Thr Val
 1 5 10 15
 His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp
 20 25 30
 Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
 35 40 45
 Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu Asp Ala Pro
 50 55 60
 Leu Glu His Val Glu Arg Phe Phe Gln Lys Met Asp Arg Asn Gln Asp
 65 70 75 80
 Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln Lys Asp Glu
 85 90 95
 Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
 100 105

<210> 35
 <211> 2644
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (49)..(816)

<400> 35
 cgggtccaa agcgggaaga ttatggacg tcccttcag cagcagag atg cag agg 57
 Met Gln Arg
 1
 acc aag gaa gcc gtg aag gca tca gat ggc aac ctc ctg gga gat cct 105
 Thr Lys Glu Ala Val Lys Ala Ser Asp Gly Asn Leu Leu Gly Asp Pro
 5 10 15
 ggg tca tca cca ctc aat aat aat taa aat att aat ttt tta aat cca 133
 Gly Arg Ile Pro Leu Ser Lys Arg Glu Ser Ile Lys Trp Gln Arg Pro
 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

gag tca tca cca ctc aat aat aat taa aat att aat ttt tta aat cca
 Gly Arg Ile Pro Leu Ser Lys Arg Glu Ser Ile Lys Trp Gln Arg Pro

gag tta taa aag gtg ggc cat cag caa gag ggc ttg gac cag cta caa 292
Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp Gln Leu Gln
70 75 80

ggt cag acc aag ttc acc aag aag gag ctg cag tcc ctt tac cga ggc 345
Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu Tyr Arg Gly
85 90 95

ttc aag aat gag tgt ccc aca ggc ctg gtg gat gaa gac acc ttc aaa 393
Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp Thr Phe Lys
100 105 110 115

ctc att tat tcc cag ttc ttc cct cag gga gat gcc acc acc tat gaa 441
Leu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ala Thr Thr Tyr Ala
120 125 130

cac ttc ctc ttc aat gcc ttt gat ggt gat ggg aac ggg gcc atc cac 489
His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly Ala Ile His
135 140 145

ttt gag gac ttt gtg gtt ggg ctc tcc atc ctg ctt cga ggg aag gtc 537
Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg Gly Thr Val
150 155 160

cat gag aag ctc aag tgg gcc ttc aat ctc tat gac att aac aag gat 585
His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp
165 170 175

ggt tgc atc acc aag gag gag atg ctg gcc atc atg aag tcc atc tac 633
Gly Cys Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
180 185 190 195

gac atg arg ggc cgc cac acc tac ccc atc ctg cgg gag gat gca ccc 681
Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu Asp Ala Pro
200 205 210

ctg gag cat gtg gag agg ttc ttt cag aaa atg gac agg aac cag gat 729
Leu Glu His Val Glu Arg Phe Phe Gln Lys Met Asp Arg Asn Gln Asp
215 220 225

gga gtg gta acc att gat gaa ttt ctg gag act ttt cag aag gat gag 777
Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln Lys Asp Glu
230 235 240

acc atc atc aac ttc atg cag ctg ttt gaa acc gtt atc aggaagg 807
Asn Ile Met Asn Ser Met Gln Leu Phe Glu Asn Val Ile
245 250 255

gggaggggac cccagtggtc attgcttctc aacccagaga agcctcaatc ctgacaggag 886

aagctctat gagaaacatt ttctaaatc atttcaaaaa agtgaggcag ttactcaca 946

ggagatcaaa	ctatcccttg	cctatgggac	catgctctt	ggagctcc	agaaatca	1346
aggggacaaa	gagggagag	gtctatagga	agaaatggt	ttgggaagctg	ggcttgagc	1366
cttatgctaa	tgatcccttg	gggtccctgga	acccgagtg	caggctacct	actatgcct	1386
gagcttagat	agtgagggg	cattggacta	agacctctg	taagagtggg	gcaggattga	1426
ggtttttgga	gaaactgagg	aaacaatttg	tccataccac	tgggtgaaga	ctgctggcca	1486
gtgggaatgt	ggctggtyga	gatttcccaa	cttcacagac	caggatggcc	tctccaaggt	1546
cctctttgat	tccctgggga	gatcacctgg	ctcatagact	gacaaccagg	gaactgggct	1606
gaaatgggag	gtctggtagg	gggcacccc	ctccttttcc	ctggccactt	gccaccagt	1666
tccttaacac	agtggatcgg	ccacacctct	gtggtctgcc	ttgaacagac	tcctcccgac	1726
caagacaaaa	aagcacaaac	tcctagcagc	tcaggccaag	cccacaaagg	aaggccctggg	1786
tcctcgagc	cctgattcag	tggccgagga	agacgtccag	acatccatcc	tgtacctcgg	1846
agccttgggg	gtctcacagc	cctttccacg	cccagctcgc	caacattcta	aagcacaaac	1906
ctggcgattc	tgcttgcttg	ggctggcccc	tggggattga	aggccactgt	taaccctaag	1966
ctggagctag	cctcgagggc	tggggacctg	tgaaccagca	acaggtcagc	agaccctcag	2026
gaggagagag	agctgttcc	gcctccacag	gcctcgccca	gaaggaaacg	tgtcccaaga	2086
agcatgttc	ctggaggaac	atccccacaa	aagtacattc	cctcatctga	agccgggtct	2146
ctgctcaggg	ctgcctctga	aagtcacgt	gtgttcccca	gaaggccagc	cccagataa	2206
gggaggctct	tagaggaaag	acagggtgac	aaacccccta	tacacagggtg	gacccccct	2266
ctgaggactg	tactgacccc	atctccatcc	tgaacggggc	cttcccttcc	cggatctaca	2326
gaaccaccagt	tctccctgga	tcagggaacc	cctgtccccc	agtctgaact	ttcccatcga	2386
ggtccctgtc	ttgtgaaaag	ccaaggccac	gggaaaaggc	caccactcta	acctggtgca	2446
tccttlagcc	cttggtgga	ggcccaacct	ggagggtct	gtcccttttg	cagggaacga	2506
actggggtg	ctccctccac	ctccctccac	ctccctccac	ctccctccac	ctccctccac	2566
ctctgtctca	ggcccaacaa	atattcagtc	ctatatattt	taataaaaga	aatttgacaa	2626
agggaaaaaa	aaaaaa					2644

(210) 36
(211) 256

Gly Asp Pro Gly Arg Ile Pro Leu Ser Lys Arg Glu Ser Ile Lys Trp
 20 25 30
 Gln Arg Pro Arg Phe Thr Arg Gln Ala Leu Met Arg Cys Cys Leu Ile
 35 40 45
 Lys Trp Ile Leu Ser Ser Ala Ala Pro Gln Gly Ser Asp Ser Ser Asp
 50 55 60
 Ser Glu Leu Glu Leu Ser Thr Val Arg His Gln Pro Gln Gly Leu Asp
 65 70 75 80
 Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu
 85 90 95
 Tyr Arg Gly Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp
 100 105 110
 Thr Phe Lys Leu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ala Thr
 115 120 125
 Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly
 130 135 140
 Ala Ile His Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg
 145 150 155 160
 Gly Thr Val His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile
 165 170 175
 Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys
 180 185 190
 Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
 195 200 205
 Asp Ala Pro Leu Glu His Val Glu Arg Phe Phe Gln Lys Met Asp Arg
 210 215 220
 Asn Gln Asp Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln
 225 230 235 240
 Lys Asp Glu Asn Ile Met Asn Ser Met Gln Leu Phe Glu Asn Val Ile
 245 250 255

210 17
 211 531
 212 DNA
 213 Homo sapiens

220
 221 CDS

222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527
 528
 529
 530
 531
 532
 533
 534
 535
 536
 537
 538
 539
 540
 541
 542
 543
 544
 545
 546
 547
 548
 549
 550
 551
 552
 553
 554
 555
 556
 557
 558
 559
 560
 561
 562
 563
 564
 565
 566
 567
 568
 569
 570
 571
 572
 573
 574
 575
 576
 577
 578
 579
 580
 581
 582
 583
 584
 585
 586
 587
 588
 589
 590
 591
 592
 593
 594
 595
 596
 597
 598
 599
 600
 601
 602
 603
 604
 605
 606
 607
 608
 609
 610
 611
 612
 613
 614
 615
 616
 617
 618
 619
 620
 621
 622
 623
 624
 625
 626
 627
 628
 629
 630
 631
 632
 633
 634
 635
 636
 637
 638
 639
 640
 641
 642
 643
 644
 645
 646
 647
 648
 649
 650
 651
 652
 653
 654
 655
 656
 657
 658
 659
 660
 661
 662
 663
 664
 665
 666
 667
 668
 669
 670
 671
 672
 673
 674
 675
 676
 677
 678
 679
 680
 681
 682
 683
 684
 685
 686
 687
 688
 689
 690
 691
 692
 693
 694
 695
 696
 697
 698
 699
 700
 701
 702
 703
 704
 705
 706
 707
 708
 709
 710
 711
 712
 713
 714
 715
 716
 717
 718
 719
 720
 721
 722
 723
 724
 725
 726
 727
 728
 729
 730
 731
 732
 733
 734
 735
 736
 737
 738
 739
 740
 741
 742
 743
 744
 745
 746
 747
 748
 749
 750
 751
 752
 753
 754
 755
 756
 757
 758
 759
 760
 761
 762
 763
 764
 765
 766
 767
 768
 769
 770
 771
 772
 773
 774
 775
 776
 777
 778
 779
 780
 781
 782
 783
 784
 785
 786
 787
 788
 789
 790
 791
 792
 793
 794
 795
 796
 797
 798
 799
 800
 801
 802
 803
 804
 805
 806
 807
 808
 809
 810
 811
 812
 813
 814
 815
 816
 817
 818
 819
 820
 821
 822
 823
 824
 825
 826
 827
 828
 829
 830
 831
 832
 833
 834
 835
 836
 837
 838
 839
 840
 841
 842
 843
 844
 845
 846
 847
 848
 849
 850
 851
 852
 853
 854
 855
 856
 857
 858
 859
 860
 861
 862
 863
 864
 865
 866
 867
 868
 869
 870
 871
 872
 873
 874
 875
 876
 877
 878
 879
 880
 881
 882
 883
 884
 885
 886
 887
 888
 889
 890
 891
 892
 893
 894
 895
 896
 897
 898
 899
 900
 901
 902
 903
 904
 905
 906
 907
 908
 909
 910
 911
 912
 913
 914
 915
 916
 917
 918
 919
 920
 921
 922
 923
 924
 925
 926
 927
 928
 929
 930
 931
 932
 933
 934
 935
 936
 937
 938
 939
 940
 941
 942
 943
 944
 945
 946
 947
 948
 949
 950
 951
 952
 953
 954
 955
 956
 957
 958
 959
 960
 961
 962
 963
 964
 965
 966
 967
 968
 969
 970
 971
 972
 973
 974
 975
 976
 977
 978
 979
 980
 981
 982
 983
 984
 985
 986
 987
 988
 989
 990
 991
 992
 993
 994
 995
 996
 997
 998
 999
 1000

```

aac gag gtg gaa agc att tgc gct caa ctg gag gag ggc agc tct aca 47
His Glu Val Glu Ser Ile Ser Ala Gln Leu Glu Glu Ala Ser Ser Thr
1 5 10 15

ggc ggt ttc ctg tac gct cag aac agc acc aag cgc agc att aac gag 96
Gly Gly Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser Ile Lys Glu
20 25 30

agg ctg atg aag ctg ttg ccc tgc tca gct gcc aaa acg tgc tct cct 144
Arg Leu Met Lys Leu Leu Pro Cys Ser Ala Ala Lys Thr Ser Ser Pro
35 40 45

gct att caa aac agc gtg gaa gat gaa ctg gag atg gcc acc gtc agg 192
Ala Ile Gln Asn Ser Val Glu Asp Glu Leu Glu Met Ala Thr Val Arg
50 55 60

cat cgg ccc gaa gcc ctt gag ctt ctg gaa gcc cag agc aaa ttt acc 240
His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys Phe Thr
65 70 75 80

aag aaa gag ctt cag atc ctt tac aga gga ttt aag aac gta aga act 288
Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Val Arg Thr
35 40 45

ctc ttt ttg act tta cct tca cac aat tcc cag agg agc att gag aaa 336
Phe Phe Leu Thr Leu Pro Ser His Asn Ser Gln Arg Ser Ile Glu Lys
100 105 110

cgagaggaaa aggggggaaaa tatcccatto tatgagaagc cccatcatat gtatatttca 396

tactgatcct tccagatag gaatataatc agtatctgtg gaatttgaat ctctgtggca 456

caccatgct ggcatactgt aattgcccac taaacaaaana gtttttgaga aaaaaaaaaa 516

aaaaaaaaaa aaaaaa 531

```

<210> 38
 <211> 112
 <212> PRT
 <213> Homo sapiens

```

<400> 38
His Glu Val Glu Ser Ile Ser Ala Gln Leu Glu Glu Ala Ser Ser Thr
1 5 10 15

Gly Gly Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser Ile Lys Glu
20 25 30

Arg Leu Met Lys Leu Leu Pro Cys Ser Ala Ala Lys Thr Ser Ser Pro
35 40 45

Ala Ile Gln Asn Ser Val Glu Ser Glu Leu Glu Met Thr Val Thr Thr
50 55 60

```

Y Gly His Leu Glu Ile Leu Tyr Arg Arg Thr Lys Asn Thr Arg Thr

Phe Phe Leu Thr Leu Pro Ser His Asn Ser Gln Arg Ser Ile Glu Lys
100 105 110

<210> 39
<211> 2176
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(124)

<400> 39
1 gaa agg ttc ttc gag aaa atg gac cgg aac cag gat ggg gta gtg acc 40
Glu Arg Phe Phe Glu Lys Met Asp Arg Asn Gln Asp Gly Val Val Thr
1 5 10 15

att gaa gag ttc ctg gag gcc tgt cag aag gat gag aac atc atg agc 47
Ile Glu Glu Phe Leu Glu Ala Cys Gln Lys Asp Glu Asn Ile Met Ser
20 25 30

tcc atg cag ctg ttt gag aat gtc atc taggacacgt ccaaaggagt 144
Ser Met Gln Leu Phe Glu Asn Val Ile
35 40

gcattggccac agccacctcc acccccaga aacctccatc ctgccaggag cagctccaa 104

gaaactttta aaaaatagat ttgaaaaag tgaacagatt gctacacaca cacacacaca 164

cacacacaca cacacacaca cacagcatt catctggggt ggcagagggg acagagtcca 224

gggagggggt gaggctgggt aggggcagag tccaggagcc ccagccagcc ctcccaggc 284

cagcgaggcg aggtctgcctc tgggtgagtg gctgacagag caggtctgca ggcaccagc 344

tgctggatgt caccagaag ggctctgagt gccctgcag gggagggctc aatctccgtt 404

gtgagccac ctgctccgtt tctccattct gctttcttgc cacacagtgg gccggcccca 464

ggctcccttg gtctctccc cgtagccact ctctgccac tacctatgct tctagaaagc 524

ccctacctc aggaacccag agggacccag tggggggcag ggggagaggg gggtaatgga 584

ggttaactt gaggcttctt ggaattctt cctgggggt cccaggatc cttctactc 644

cattgacctg gaagagctgg gtaccaggcc acccactgtg gggcaagcct gagtggtgag 704

gggcaactgg gccccattct cctccatggt caggaaggcg ggggatttca agtttaggga 764

ctgtctgtg gtggagaatc ctgggacac ctctgagag ctacacaggt gggatgagc 824

tatcttctc cagtctctt ctctctctt ctctctctt ctctctctt ctctctctt 884

ctctctctt ctctctctt ctctctctt ctctctctt ctctctctt ctctctctt 944

ctctctctt ctctctctt ctctctctt ctctctctt ctctctctt ctctctctt 1004

ctctctctt ctctctctt ctctctctt ctctctctt ctctctctt ctctctctt 1064

cctagtggga gcccagcaca ctgtttctcg gaggccagga cctcctgctg gctgaggctt 1284
 gggcccagta gcccacatat ggtggccctg gggaagagga cttggggggtc tctctctgtg 1344
 ctgggatcag tggggcccca agcccagcc cggctgacca acattcaaaa gcacaaaacc 1404
 tgggjaetct gcttggtgtt cccctccatc tggggatgga gaatgcacgc ccaagctgg 1464
 agccatggt gaggctgag agggctgtgg ctgggtggtc agcagaaaa cccaggagga 1524
 gagatctgt gctcccgctt gattgggggc tcaccagaa ggaaccgggt cccaggagga 1584
 atggccctc caggaacatt cccacataat acattccatc acagccagcc cagctccact 1644
 caggcttggc cgggggagtc cccgtgtgcc ccaagaggtt agcccaggg ttagcagggc 1704
 cctcagagga aaggcagtat ggcggaggcc atggggggcc ctgggcattc acacacagcc 1764
 tggctccccc tgggagctg catggagccc tggctccagg ctccaggctg actgggggccc 1824
 tctgtctcca ggagggcata agctttccct ggctcaggga tcttctccct cccctccccc 1884
 gctgcccagc cctccagctt ggtgtccatc tgcctctaag gccaaggcct caggagagca 1944
 tcacacccac acccctgcgc gcttggcctt tggggccaga ctggctgcac agcccaccca 2004
 ggaggggtct gctcccaag ctgggacaca gacgggcgc atgtctgcac ggcagaagcg 2064
 tctccgttgg ccacggcctg ggagggtgtt tctgttctc agcatccact aatattcagt 2124
 cctgtatatt ttaataaaat aaacttgaca aaggaaaaaa aaaaaaaaaa aa 2176

<210> 40
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 40
 Glu Arg Phe Phe Glu Lys Met Asp Arg Asn Gln Asp Gly Val Val Thr
 1 5 10 15
 Ile Glu Gln Phe Leu Glu Ala Cys Gln Lys Asp Glu Asn Ile Met Ser
 20 25 30 35
 Ser Met Gln Leu Phe Glu Asn Val Ile
 35 40

<210> 41
 <211> 2087
 <212> DNA

<4> 41

tctctaaaga aaagccttgc cagccctctac tccgggcccc caacccccagc aggtcagctgc 126

ggcgccaggg ggagctgtgt gagcgcccta ttctggccac cgggggcccc ctcccaaggg 186

ccaggcgggga gggggggccc gggggccc atg cgg ggc caa ggc aga aag gag agt 234

Met Arg Gly Gln Gly Arg Lys Glu Ser

1

5

ttg tcc gaa tcc cga gat ctg gac ggc tcc tat gac cag ctt acg ggc 282

Leu Ser Glu Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly

10

15

20

25

cac cct cca ggg ccc agt aaa aaa gcc ctg aag cag cgt ttc ctc aag 330

His Pro Pro Gly Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys

30

35

40

ctg ctg ccg tgc tgc ggg ccc caa gcc ctg ccc tca gtc agt gaa aac 378

Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Asn

45

50

55

agc gta gag gat gag ttt gaa tta tcc aag gtg tgt cac cga cct gag 426

Ser Val Glu Asp Glu Phe Gln Leu Ser Thr Val Cys His Arg Pro Glu

60

65

70

ggc ctg gaa caa ctc cag gaa cag acc aag ttc aca cgc aga gag ctg 474

Gly Leu Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu

75

80

85

cag gtc ctg tac cga gcc ttc aag aac gaa tgc ccc agt ggg att gtc 522

Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val

90

95

100

105

aac gag gag aac ttc aag cag att tat tct cag ttc ttc ccc caa gga 570

Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly

110

115

120

gac tcc agc aac tat gct act ttc ctc ttc aat gcc ttt gac acc aac 618

Asp Ser Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn

125

130

135

cac gat ggc tct gtc agt ttt gag gac ttt gtc gct ggt ttg tgg gtc 666

His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val

140

145

150

att ctt cga ggg acc ata gat gat aat cta aat tgg act ttc aat tta 714

Ile Leu Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu

155

160

165

tat gac ctc aac aag gac ggc tgt atc aca aag gag gaa atg ctt gac 762

Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp

170

175

180

185

ctc att att att att att att att att att att att att att att att att 782

Leu Arg Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu

190

195

200

atg gac agg aac aag gac ggc gtg gtg acc atc gag gaa ttc atc gag 905
 Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu
 220 225 230
 tct tgt caa cag gac gag aac atc atg agg tcc atg cag ctc tca ccc 914
 Ser Cys Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu Ser Pro
 235 240 245
 ctt ctc aac tgatacctag tgctgaggac acccctggtg tagggaccaa 1003
 Leu Leu Asn
 250
 gtgggtctctcc acctttctagt cccactctag aaaccacatt agacagaagg tctcctgcta 1063
 tgggtgcttcc cccatcccta atctcttaga tttctctcaa gactcccttc tca-gagaaca 1113
 cgtctgtctcc atgtcccccag ctgggtctctc agcctagcct ttgaggggccc tgtggggagg 1163
 cgggggacaag aaagcagaaa agtcttgggc ccgagccagt ggttaggtcc taggaattgg 1213
 ctggagtggg ggcacagaaag cctgggcaga tgatgagagc ccagctgggc tgtcactgca 1303
 ggttcggggg cctacagccc tgggtcagca gagtatgagt tccagactt tccagaaggt 1363
 ccttagcaat gtcccagaaa ttcacogtac acctctcagt gtcttaggag ggcccgggat 1423
 ccagatgtct ggttcctccc tgaatctct cctcctctt tgcctgtatg gtgggagtgg 1483
 tggccagggg aagatgagtg gtgtcccgga tgatgcctgt caaggtccca cctccctccc 1543
 ggctgtctct atgacagctg ttgggtctct cagacccct atctagatgt agaggcatgg 1603
 agtgagtccg ggattcccg aaattgagtt ttacacctcc tctagtggc tgccttaggg 1663
 gaatgggaag aacccagtgt gggggcacc attagaatct ttgcocggct cctcacaatg 1723
 ccttagggtc ccttagggta ccogctccct ctgttttagtc taaccagaga tgcctctgag 1783
 ctacactaga ggytagggac ggtaggctcc aggtccaacc tctccaggtc agcaccctgc 1843
 catgtgtctg ctctcatta acaaacctgc ttgtctcttc ctgcgcctct tctcagtcag 1903
 ccaaggctct aggggaaggg ctccagttt cccatccgt cagacatggt cgaatgctt 1963
 gcaatctgt cctctctt tctctctta cctcagat cagatctat aacatctg 2023
 gctatgcaca aaaaaaaaaa aaaaaaaaaa aaaa 2057

<210> 42
 <211> 252
 <212> FRT
 <213> Ratius, et al.

Atty. Docket No.: MNI-070CP4
 Rhodes, Kenneth, et al.

Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Glu Asp Glu Phe Glu
 50 55 60
 Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
 65 70 75 80
 Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe
 85 90 95
 Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
 100 105 110
 Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr Ala Thr
 115 120 125
 Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 130 135 140
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp
 145 150 155 160
 Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
 165 170 175
 Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
 180 185 190
 Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
 195 200 205
 Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
 210 215 220
 Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp Glu Asn
 225 230 235 240
 Ile Met Arg Ser Met Gln Leu Ser Pro Leu Leu Asn
 245 250

<210> 43

<211> 26

<212> FRT

<213> Artificial Sequence

<220>

<221> misc_feature

<222> 2,5,6,9,17,25,26

<223> Met, Ile, Leu, Val, Lys, Met

<224>

<225> Description of Artificial Sequence: sequence

<400> 43

Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Asp Gly Asp Gly Xaa
1 5 10 15Xaa Xaa Xaa Xaa Glu Phe Xaa Xaa Xaa Xaa
20 25

<210> 44

<211> 40

<212> DNA

<213> Rattus sp.

<410> 44

taa'acgact cactataggg actggccatc ctgctctcag

40

<210> 45

<211> 40

<212> DNA

<213> Rattus sp.

<400> 45

attaacctc actaaaggga cactactgtt taagctcaag

40

<210> 46

<211> 40

<212> DNA

<213> Rattus sp.

<400> 46

taa'acgact cactataggg cacctccctt ccgctgttc

40

<210> 47

<211> 40

<212> DNA

<213> Rattus sp.

<400> 47

attaacctc actaaaggga gagcagcagc atggcaggt

40

<210> 48

<211> 2413

<212> DNA

<213> Simian sp.

<220>

<221> PDB

<222> 1993, 1994, 1995

The following information is provided for your information only.

The following information is provided for your information only.

aagcctgaag ttgtatgat tctgtaatta actccctcca ctccaaaggg gtctggaggg 247

tgagatgctc tgcagatcca gagg atg ttg act ctg gag tgg gag tcc gaa 291
Met Leu Thr Leu Glu Trp Glu Ser Glu
1 5

gga ctg caa aca gtg ggt att gtt gtg att ata tgt gca tct ctg aag 339
Gly Leu Gln Thr Val Gly Ile Val Val Ile Ile Cys Ala Ser Leu Lys
10 15 20 25

ctg ctt cat ttg ctg gga ctg att gat ttt tgg gaa gac agc gtg gaa 387
Leu Leu His Leu Leu Gly Leu Ile Asp Phe Ser Glu Asp Ser Val Glu
30 35 40

gat gaa ctg gag atg gcc act gtc agg cat cgg cct gag gcc ctt gag 435
Asp Glu Leu Glu Met Ala Thr Val Arg His Arg Pro Glu Ala Leu Glu
45 50 55

ctt ctg gaa gcc cag agc aaa ttt acc aag aaa gag ctt cag atc ctt 483
Leu Leu Glu Ala Gln Ser Lys Phe Thr Lys Lys Glu Leu Gln Ile Leu
60 65 70

tac aga gga ttt aag aac gaa tgc ccc agt ggt gtt gtt aat gaa gaa 531
Tyr Arg Gly Phe Lys Asn Gln Cys Pro Ser Gly Val Val Asn Glu Glu
75 80 85

acc ttc aaa gag att tac tgg cag ttc ttt cca cag gga gac tct aca 579
Thr Phe Lys Glu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Thr
90 95 100 105

aca cat gca cat ttt ctg ttc aat ggg ttt gat aag gac cac aat gga 627
Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Thr Asp His Asn Gly
110 115 120

gct gtg agt ttc gag gat ttc atc aaa ggt ctt tcc att tgg ctc cgg 675
Ala Val Ser Phe Glu Asp Phe Ile Lys Gly Leu Ser Ile Leu Leu Arg
125 130 135

ggg aca gta caa gaa aaa ctc aat tgg gca ttt aat ctg tat gat ata 723
Gly Thr Val Gln Glu Lys Leu Asn Trp Ala Phe Asn Leu Tyr Asp Ile
140 145 150

aat aaa gat ggc tac atc acc aaa gag gaa atg ctt gat ata atg aaa 771
Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys
155 160 165

gca ata tac gac atg atg ggt aaa tgt aca tat cct gtc ctc aaa gaa 819
Ala Ile Tyr Asp Met Met Gly Lys Cys Thr Tyr Pro Val Leu Lys Glu
170 175 180 185

gat gca ccc aga caa caa gtc gaa aca ttt ttt aag aaa atg gac aaa 867
Asp Ala Pro Arg Gln His Val Glu Thr Phe Phe Gln Lys Met Asp Lys
190 195 200 205

atg atg gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa 915
Ile Arg Glu Arg Ile Met Arg Arg Met Arg Arg Arg Arg Arg Arg Arg

taacttgtea actagatent gaatccaaca gacaaatgtg aactattota ccacotttaa 1023
agtcggagot accactttta gcatagattg ctacagcttga caatgaagca tattatgcaa 1083
acaagctttg ttttaatat aagcaatccc caaaaagattt gagttttota gttataaatt 1143
tgcactcttt ccataatgoc actgagttca tgggatgttc taactcattt catactctgt 1203
gaatattcaa aagtaataga atctggcata tagttttatt gattccttag ccacgggatt 1263
attgaggott tcatatatca gtgattttta aataccagtg ttttttgctc tcatttctat 1323
gtattcagtc ctaggatttt gaatggtttt ctaatatact gacatctgca ttttaatttc 1383
agaaattaaa ttaattttca tgtctgaatg ctgtaattcc atttatatac ttttaagtaaa 1443
caataaagat tactacaatt aaacacatag ttccagtctc tatggccttc ccttcccacc 1503
ttctattata aattaatttt atctgggtat ttttaacatt taactattta tcatcagata 1563
tcagcatatg cctaattatg cctaattgaaa ctttaataagc atttaatttt ccacatatac 1623
ctatagccaa ggcctatata ctatatataa tcttggtatt gtttaatttt acaggctgtt 1683
ttccattgta tcatcaagtg gaagtccaag acgggcacaa acaaaaacag gatgtttaca 1743
gacatctgca aagggctcagg atatctatcc tccagtatat gttaatgctt aataacaagt 1803
aatcctaaca gcattaaagg ccaaatctgt cctctttccc ctgacttctc tacagcatgt 1863
ttatattaca agcattcag ggacaaaagaa accttgacta ccccatgtc tactaggaac 1923
aaacaaaacg caagcaaaat tcactttgaa agcaccagtg gttccatnac attgacaact 1983
actaccaaga ttcagtagaa aataagtgtc caacaactaa tccagatnac aatatgattt 2043
agtgcacat aaaattccaa caattcagat tatttttaat catctcagcc acaactgtaa 2103
agttgcacac ttaactaaaga cacacacatc gtccctgttt tctagaaata tcacaaagac 2163
caagaggcta cagaaggagg aaattttgca ctgtcttttc aacaataaat caggtatota 2223
ttctggtgta gacataagat gtgaaagct cctctgtctt ccccatctca gaatttaaa 2283
gtagacaaat caatgaaac ttaattttc cactctctt tgggtaaa ttaattgtga 2343
cattttgtat ttcaaaaaga aaaaataaaa gcaaaataaa atgttwawaa mwmwaaaaaa 2403
aaaaaaaaa 2413

210-48

210-48

210-48 210-48 210-48 210-48 210-48 210-48 210-48 210-48

Val Val Ile Ile Cys Ala Ser Leu Lys Leu Leu His Leu Leu Gly Leu
20 25 30
Ile Asp Phe Ser Glu Asp Ser Val Glu Asp Glu Leu Glu Met Ala Thr
35 40 45
Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys
50 55 60
Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Glu
65 70 75 80
Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr Ser
85 90 95
Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe
100 105 110
Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe
115 120 125
Ile Lys Gly Leu Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys Leu
130 135 140
Asn Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Thr
145 150 155 160
Lys Glu Glu Met Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly
165 170 175
Lys Cys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val
180 185 190
Glu Thr Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Val Val Thr
195 200 205
Ile Asp Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn Ile Met Arg
210 215 220
Ser Met Gln Leu Phe Glu Asn Val Ile
225 230

<110> 50
<111> 1541
<112> DNA
<113> Simian sp.

<220>
<221> CDS
<222> (265)...(963)

tgggatgacc tgcagatcca gagg atg ttg act ctg gag tgg gac tcc gaa 291
Met Leu Thr Leu Glu Trp Glu Ser Glu
1 5

gga ctg caa aca gtg ggt att gtt gtg att ata tgt gca tct ctg aag 339
Gly Leu Gln Thr Val Gly Ile Val Val Ile Ile Cys Ala Ser Leu Lys
10 15 20 25

ctg ctt cat ttg ctg gga ctg att gat ttt tgg gaa gac agc gtg gaa 387
Leu Leu His Leu Leu Gly Leu Ile Asp Phe Ser Glu Asp Ser Val Glu
30 35 40

gat gaa ctg gag atg gcc act gtc agg cat cgg cct gag gcc ctt gag 435
Asp Glu Leu Glu Met Ala Thr Val Arg His Arg Pro Glu Ala Leu Glu
45 50 55

ctt ctg gaa gcc cag agc aaa ttt acc aag aaa gag ctt cag atc ctt 483
Leu Leu Glu Ala Gln Ser Lys Phe Thr Lys Lys Glu Leu Gln Ile Leu
60 65 70

tac aga gga ttt aag aac gaa tgc ccc agt ggt gtt gtt aat gaa gaa 531
Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val Val Asn Glu Glu
75 80 85

acc ttc aaa gag att tac tgg cag ttc ttt cca cag gga gac tct aca 579
Thr Phe Lys Glu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Thr
90 95 100 105

aca tat gca cat ttt ctg ttc aat gag ttt gat acg gac cac aat gga 627
Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Thr Asp His Asn Gly
110 115 120

gct gtg agt ttc gag gat ttc atc aaa ggt ctt tcc att ttg ctc cgg 675
Ala Val Ser Phe Glu Asp Phe Ile Lys Gly Leu Ser Ile Leu Leu Arg
125 130 135

ggg aca gca caa gaa aaa ctc aat tgg gca ttt aat ctg tat gat ata 723
Gly Thr Val Gln Glu Lys Leu Asn Trp Ala Phe Asn Leu Tyr Asp Ile
140 145 150

aat aaa gat ggc tac atc act aaa gag gaa atg ctt gat ata atg aaa 771
Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys
155 160 165

aca ata tat gat atg atg gpt aaa ttt aca tat ctt ttt ttt aaa gaa 819
Ala Ile Tyr Asp Met Met Gly Lys Cys Thr Tyr Pro Val Leu Lys Glu
170 175 180 185

gat gca ccc aga caa cac gtc gaa aca ttt ttt cag gct gtt ttc cat 867
Asp Ala Pro Arg Gln His Val Glu Thr Phe Phe Gln Ala Val Thr His
190 195 200

ctt gca ttt atg ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 915
Leu Leu Arg Ile Tyr Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
205 210 215 220 225 230 235 240 245 250

taatgcttaa taacaagtaa tccaaacaga attaaaggcc aaatctgtcc tctttccctt 1023
 gaattcctta cagcatgttt atattacaag ccattcaggg acaaagaaac ctggaactac 1083
 ccactgtcta ctaggaaaca acaaacagca agcaaaattc actttgaaag cactagtggt 1143
 tccattacat tgacaactac taccagatt cagtagaaaa taagtgtcca acaactaatc 1203
 cagattacaa tatgatttag tgcacataa aattccaaca attcagatta tttttaatca 1263
 tctcagccac aactgtaaag ttgcacatt actaaagaca cacacatcgt cctgtgtttg 1323
 tagaatatc acaaagacca agaggctaca gaaggaggaa atttgcaact gtctttgcaa 1383
 caataaatca ggtatctatt ctgggtgtaga gataggatgt tgaaagctgc cctgctatca 1443
 ccagtgtaga aattaagagt agtacaatac atgtacactg aaatttgcca tgcgtgtttt 1503
 gtgtaaactc aatgtgcaca ttttgtatct caaaaagaaa aaataaaagc aaaataaat 1563
 gttwawaamw mwaaaaaaaa aaaaaaaaaa 1591

(210): 51
 (211): 233
 (212): PRT
 (213): Simian sp.

(400): 51
 Met Leu Thr Leu Glu Trp Glu Ser Glu Gly Leu Gln Thr Val Gly Ile
 1 5 10 15
 Val Val Ile Ile Cys Ala Ser Leu Lys Leu Leu His Leu Leu Gly Leu
 20 25 30
 Ile Asp Phe Ser Glu Asp Ser Val Glu Asp Glu Leu Glu Met Ala Thr
 35 40 45
 Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys
 50 55 60
 Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Glu
 65 70 75 80
 Cys Pro Ser Gly Val Val Asn Gln Gln Thr Phe Lys Glu Ile Tyr Ser
 85 90 95
 Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe
 100 105 110
 Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Gln Asp Phe
 115 120 125

13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120

Lys Lys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val
180 185 190

Glu Thr Phe Phe Gln Ala Val Phe His Cys Ile Ile Lys Trp Lys Phe
195 200 205

Lys Thr Ala Ser Asn Lys Thr Arg Met Phe Thr Asp Ile Cys Lys Gly
310 215 220

Ser Gly Tyr Leu Ser Ser Ser Ile Cys
225 230

0210 - 42
0211 - 2051
0212 - DNA
0213 - Rattus sp.

- 0.120
- 0.121 - CDS
- 0.122 - (85) .. (1305)

gaggaacta agcaactact ggggtggtgc cctgggtctg caqagaacaa gaaaagcttc 60

tctggcagggc tgtcagctgc caaa atg aac ggc gtg gaa ggg aac aac gag 111
 Met Asn Gly Val Glu Gly Asn Asn Glu
 1 5

Phe Val Phe Gly Ala Ala Arg Ala Ser Gln Ser Gln Gln Gln Gln Gln 159
 Leu Pro Leu Ala Asn Thr Ser Thr Ser Ala Leu Val Pro Glu Asp Leu
 10 15 20 25

207
 Asp Leu Lys Gln Asp Gln Pro Leu Ser Glu Glu Thr Asp Thr Val Arg
 30 35 40

-gag atg gag gct gca ggt gag gcc ggt gag gag gga ggc gcg tcc ccc 255
Glu Met Glu Ala Ala Gly Glu Ala Gly Ala Glu Gly Gly Ala Ser Pro
 45 50 55

Glu Tyr GAG GAC TGC GAG GCG CAG CTC TGC CTC CGA GTG GGT GAG AAT 303
Asp Ser Glu His Cys Asp Pro Gln Leu Cys Ser Arg Val Ala Glu Asn

64 68 72

ggg tgg gat ggc gca gag gga gag ggg ctg gag gat ggt ctg tct tca 351
Gly Cys Ala Ala Ala Ala Gly Glu Gly Leu Glu Asp Gly Leu Ser Ser
75 80 85

Ser Lys Cys Gly Asp Ala Pro Leu Ala Ser Val Ala Ala Asn Asp Ser

[illegible]

cca ggg cgg aag aag acc aag gta atg act acc aag ggc gcc atc tat 543
 Pro Gly Pro Lys Lys Thr Lys Val Met Thr Thr Lys Gly Ala Ile Ser
 140 145 150

gcg act acc ggc aag gaa gra gaa gca ggg gcg gca atc cag gaa aag 591
 Ala Thr Thr Gly Lys Glu Gly Glu Ala Gly Ala Ala Met Gln Glu Lys
 155 160 165

aag ggg gtg cag aaa gaa aaa aag gca gct gga gga ggg aaa gac gac 639
 Lys Gly Val Gln Lys Glu Lys Lys Ala Ala Gly Gly Gly Lys Asp Glu
 170 175 180 185

act cgt cct aga gcc cct aag atc aat aac tgg atg gac tcc ctg gaa 687
 Thr Arg Pro Arg Ala Pro Lys Ile Asn Asn Cys Met Asp Ser Leu Glu
 190 195 200

gcc atc gat caa gag ctg tca aat gta aat gcg caa gct gac agg gcc 735
 Ala Ile Asp Gln Glu Leu Ser Asn Val Asn Ala Gln Ala Asp Arg Ala
 205 210 215

ttc ctg cag ctg gaa cgc aaa ttt ggg cgg atg aga agg ctg cac atg 783
 Phe Leu Gln Leu Glu Arg Lys Phe Gly Arg Met Arg Arg Leu His Met
 220 225 230

cag cgc cga agt ttc atc atc caa aac atc cca ggt ttc tgg gtc acc 831
 Gln Arg Arg Ser Phe Ile Ile Gln Asn Ile Pro Gly Phe Trp Val Thr
 235 240 245

gcg ttt cgg aac caa cgg caa ctg tca cgg atg atc agt gcc caa gat 879
 Ala Phe Arg Asn His Pro Gln Leu Ser Pro Met Ile Ser Gly Gln Asp
 250 255 260 265

gaa gac atg atg agg tac arg atc aat tta gag gtc gag gag ctt aag 927
 Glu Asp Met Met Arg Tyr Met Ile Asn Leu Glu Val Glu Glu Leu Lys
 270 275 280

cac cca aga gca ggg tgc aaa ttt aag ttc atc ttc caa agc aac ccc 975
 His Pro Arg Ala Gly Cys Lys Phe Lys Phe Ile Phe Gln Ser Asn Pro
 285 290 295

tac ttc cga aat gag cgg ctg gtc aaa gag tac gac ctc aga tcc tca 1023
 Tyr Phe Arg Asn Glu Gly Leu Val Lys Glu Tyr Glu Arg Arg Ser Ser
 300 305 310

ttt cga gtc ttt ttt ctc ttt arg caa atc ggt ttt ttt cgg ggt caa 1071
 Gly Arg Val Val Ser Leu Ser Thr Pro Ile Arg Trp His Arg Gly Gln
 315 320 325

gaa ccc cag gcc cat atc cac agg aat aga gag ggg aac agc att ccc 1119
 Glu Pro Gln Ala His Ile His Arg Asn Arg Glu Gly Asn Thr Ile Pro
 330 335 340 345

tta ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 1167
 Ile Ala Ile Ile Ile Lys Gly Glu Lys Thr Ser Asn Pro Ile Glu Tyr
 350 355 360 365

tac ctg atg ggc gat ggg cca cgg aga gga gtt cga gtc cca cca agg 1263
 Tyr Leu Met Gly Asp Gly Pro Arg Arg Gly Val Arg Val Pro Pro Arg
 330 385 390

cag cca gtg gag agt ccc agg tcc ttc agg ttc cag ttc ggc 1305
 Gln Pro Val Glu Ser Pro Arg Ser Phe Arg Phe Gln Ser Gly
 395 400 405

taagctctgc cctcgtgaga agctcttaca gaagagtcct taccaccttc tcagcttggc 1365

taggagcatg cagccttctg tatgctttct ctctcttggg ttgtgtcctt tgggtctctt 1415

aagtctcggg tagtttcaag gttgtgggtt ccaagctctt gtctctcttt ctcttggcca 1465

tcacgatgta ctgcatagt ttaatgggtg tccaagtcca tggcctccaa actgcttcta 1515

tggcaagctc acgtgtgtga gtttgtactg ctctctcttg catggcttgg tctctgtctg 1605

tgatcttcta ggttttttgt tttctttttt aaaagtgggt ctctatcaaa agaaagcttg 1665

acatctctt accaagaact agccagattt catactgtgt tcccgatct tatgtactgt 1725

gaagaactgt gagtttggcc actgcaagat gggactgtat cccaatccag ccctcagccc 1785

aacaggcat tccaagctgt caccaaactga tcttagctgt ctctctgggc ctctgccatt 1845

tacctcctt tttatctata gaatgagcag gtggtctgga ggtgactact aggttaagagt 1905

gaagtattag gtgaggagt tttctgtgca ccacattgt ctctgtacaa tgcctcatga 1965

tcagcttggg tcagctactg actgtctgat attctatacc cccaacacaa aaaaaaaaaa 2025

aaaaaaaaa aaaaaaaaaa aaaaaa 2051

4210 - 53

4211 - 407

4212 - FRT

4213 - Pattus sp.

4400 - 53

Met Asn Gly Val Glu Gly Asn Asn Glu Leu Pro Leu Ala Asn Thr Ser
 1 5 10 15

Thr Ser Ala Leu Val Pro Glu Asp Leu Asp Leu Lys Glu Asp Thr Pro
 20 25 30

Leu Ser Glu Glu Thr Asp Thr Val Arg Glu Met Glu Ala Ala Gly Glu
 35 40 45

Ala Gly Ala Glu Gly Gly Ala Ser Pro Asp Ser Glu His Cys Asp Pro
 50 55 60

11. All other DNA, RNA, and protein sequences are as described in the literature.

Ala Gly Pro Leu Ser Pro Ala Lys Pro Lys Thr Leu Glu Ala Ser Gly
115 120 125

Ala Val Gly Leu Gly Ser Gln Met Met Pro Gly Pro Lys Lys Thr Lys
130 135 140

Val Met Thr Thr Lys Gly Ala Ile Ser Ala Thr Thr Gly Lys Glu Gly
145 150 155 160

Glu Ala Gly Ala Ala Met Gln Glu Lys Lys Gly Val Gln Lys Glu Lys
165 170 175

Lys Ala Ala Gly Gly Gly Lys Asp Glu Thr Arg Pro Arg Ala Pro Lys
180 185 190

Ile Asn Asn Cys Met Asp Ser Leu Glu Ala Ile Asp Gln Glu Leu Ser
195 200 205

Asn Val Asn Ala Gln Ala Asp Arg Ala Phe Leu Gln Leu Glu Arg Lys
210 215 220

Phe Gly Arg Met Arg Arg Leu His Met Gln Arg Arg Ser Phe Ile Ile
225 230 235 240

Gln Asn Ile Pro Gly Phe Trp Val Thr Ala Phe Arg Asn His Pro Gln
245 250 255

Leu Ser Pro Met Ile Ser Gly Gln Asp Glu Asp Met Met Arg Tyr Met
260 265 270

Ile Asn Leu Glu Val Glu Glu Leu Lys His Pro Arg Ala Gly Cys Lys
275 280 285

Phe Lys Phe Ile Phe Gln Ser Asn Pro Tyr Phe Arg Asn Glu Gly Leu
290 295 300

Val Lys Glu Tyr Glu Arg Arg Ser Ser Gly Arg Val Val Ser Leu Ser
305 310 315 320

Thr Pro Ile Arg Trp His Arg Gly Gln Glu Pro Gln Ala His Ile His
325 330 335

Arg Asn Arg Glu Gly Asn Thr Ile Pro Ser Phe Phe Asn Tyr Phe Ser
340 345 350

Asp His Ser Leu Leu Glu Phe Asp Arg Ile Ala Glu Ile Ile Lys Gly
355 360 365

Glu Leu Trp Ser Asn Pro Leu Gln Tyr Tyr Leu Met Gly Asp Gly Pro
370 375 380

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (88)..(1329)

<400> 54

gggtgtgtgtg tagacgtttt gggcagagct cggcgctgtc ggaggacaag gaactctccc 60

tcctccacta gtctgacttc ttccaaa atg agc ggc atg gat ggg ggc aac aag 114
Met Ser Gly Leu Asp Gly Gly Asn Lys

1

5

ctc cct ctc gcc caa acc ggc ggc ctg gct gct ccc gac cat gcc tca 162
Leu Pro Leu Ala Gln Thr Gly Gly Leu Ala Ala Pro Asp His Ala Ser
10 15 20 25

gga gat ccc gac cta gac cag tgc caa ggg ctg cgt gaa gaa acc gag 210
Gly Asp Pro Asp Leu Asp Gln Cys Gln Gly Leu Arg Glu Glu Thr Glu
30 35 40

gcg aca cag gtg atg ggc aac aca ggt ggg ggc agc ctg gag acc gtt 258
Ala Thr Gln Val Met Ala Asn Thr Gly Gly Gly Ser Leu Glu Thr Val
45 50 55

gca gag ggg ggt gca tcc cag gat cct gtc gac tgt ggc ccc gag ctg 306
Ala Glu Gly Gly Ala Ser Gln Asp Pro Val Asp Cys Gly Pro Ala Leu
60 65 70

ggc gtc cca gtt gcc ggg agt cgc ggc ggt gca gag acc aac gcc ggg 354
Arg Val Pro Val Ala Gly Ser Arg Gly Gly Ala Ala Thr Lys Ala Gly
75 80 85

cag gag gat gct cca cct tct acg aaa ggt ctg gaa gca gcc tct gcc 402
Gln Glu Asp Ala Pro Pro Ser Thr Lys Gly Leu Glu Ala Ala Ser Ala
90 95 100 105

gcc gag gct gct gac agc agc cag aaa aat ggc tgt cag ctt gga gag 450
Ala Glu Ala Ala Asp Ser Ser Gln Lys Asn Gly Cys Gln Leu Gly Glu
110 115 120

acc agt ggc cct gct ggg cag aag gct cta gaa gcc tgt gga gca ggg 498
Pro Arg Gly Pro Ala Gly Gln Lys Ala Leu Glu Ala Cys Gly Ala Gly
125 130 135

ggc ttg ggg tct cag atg ata ccc ggg aag aag gcc aag gaa gtg acg 546
Gly Leu Gly Ser Gln Met Ile Pro Gly Lys Lys Ala Lys Glu Val Thr
140 145 150

act aac aac cct cct ctc tgg tca gca ggt tca aat gat gga gaa gga 594
Thr Lys Lys Arg Ala Ile Ser Ala Ala Val Glu Lys Glu Gly Glu Ala
155 160 165

ttt ttt ttt ttt ttt gag tat tta ttt ttt ttt ttt ttt ttt ttt ttt ttt 642
Phe Phe Phe Phe Phe Gly Tyr Trp Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe
170 175 180 185 190 195 200 205 210 215 220 225 230 235 240

aac tgc atg gac tca ctg gag gcc atc gat caa gag ttg tca aac gta 738
 Asn Cys Met Asp Ser Leu Glu Ala Ile Asp Gln Glu Leu Ser Asn Val
 205 210 215

aat gcc cag gct gac agg gcc ttc ctt cag ctt gag cgc aag ttt ggc 786
 Asn Ala Gln Ala Asp Arg Ala Phe Leu Gln Leu Glu Arg Lys Phe Gly
 220 225 230

cgc atg cga agg ctc cac atg cag cgc aga agt ttc att atc cag aat 834
 Arg Met Arg Arg Leu His Met Gln Arg Arg Ser Phe Ile Ile Gln Asn
 235 240 245

atc cca ggt ttc tgg gtt act gcc ttt cga aac cac ccc cag ctg tca 882
 Ile Pro Gly Phe Trp Val Thr Ala Phe Arg Asn His Pro Gln Leu Ser
 250 255 260 265

cct atg atc agt ggc caa gat gaa gac atg ctg agg tac atg atc aat 930
 Pro Met Ile Ser Gly Gln Asp Glu Asp Met Leu Arg Tyr Met Ile Asn
 270 275 280

ttg gag gtg gag gag ctt aaa cac ccc aga gca ggc tgc aaa ttc aag 978
 Leu Glu Val Glu Glu Leu Lys His Pro Arg Ala Gly Cys Lys Phe Lys
 285 290 295

ttc atc ctt cag ggc aac ccc tac ttc cga aat gag ggc ctt gtc aag 1026
 Phe Ile Phe Gln Gly Asn Pro Tyr Phe Arg Asn Glu Gly Leu Val Lys
 300 305 310

gaa tat gaa cgc aga tcc cct ggc cgg gtg gtg cct ctt tcc act cca 1074
 Glu Tyr Glu Arg Arg Ser Ser Gly Arg Val Val Ser Leu Ser Thr Pro
 315 320 325

atc cgc tgg cac cga ggc caa gac ccc cag gct cat atc cac aga aac 1122
 Ile Arg Trp His Arg Gly Gln Asp Pro Gln Ala His Ile His Arg Asn
 330 335 340 345

cgg gaa ggg aac act atc cct agt ttc ttc aac tgg ttt tca gac cac 1170
 Arg Glu Gly Asn Thr Ile Pro Ser Phe Phe Asn Trp Phe Ser Asp His
 350 355 360

agc ctt cta gaa ttc gac aga att gca gag att atc aaa gga gaa ctg 1218
 Ser Leu Leu Glu Phe Asp Arg Ile Ala Glu Ile Ile Lys Gly Glu Leu
 365 370 375

tgg cct aat ctt cta cta cta cta cta cta cta cta cta cta cta cta 1266
 Trp Pro Asn Pro Leu Gln Tyr Tyr Leu Met Gly Glu Gly Pro Arg Arg
 380 385 390

gga att cga ggc cca cca agg cag cca gtg gag aga ggc aga tcc ttc 1314
 Gly Ile Arg Gly Pro Pro Arg Gln Pro Val Glu Ser Ala Arg Ser Phe
 395 400 405

aaaagtcag agcaggaatg agcctgctgt ggagtgaggt tggaaaggt cacaggaaaag 3409
 aacctgcagg atcaggggtg ggaggggagg cccctgaggt gctctccagg gaagagggga 3469
 tggggtttaa atagcatgtt tggaggaaga tttctctca atttctcta agtccttgaa 3529
 ttcaccagta gattttttgta aabaaaaatgt aagtcgatgt tttctctcaa ttatcctagg 3589
 agtgaccttt atatgtgtgg aagattaatg gtatatgctt ctatgtctac tgtttttgag 3649
 taaaatccat ttcctttctt tgtttcagcc tatgacaaaa ttgatgttta caggcctgtt 3709
 ttttgcttat aattgacaa atgtgacaaa ataccaaatt tgtgtcctgt gcagtatgaa 3769
 gaattcagtg aatattcatt aatgtattag ctgtttttgc tctctgttca tatatggctt 3829
 tattcttaga aatataattt gaatgtgac tttcaatagt ctgaatattt tacaaattat 3889
 agctatgtct tgtgaaaaa acccaaaaa gaaaaataag acctgttgtt ctacttgat 3949
 attttctgct ctagtaattg acttgacatt tatgttcta agcagtgtaa gtaccagtag 4009
 aattctctg tcaaaactaa tgatcattta gtactttgt ctctctccat gtgcttgaag 4069
 gaaaaataaa gtgtcactac cgtatttctt gttttcatca aaaaaataaaa ataatttaaa 4129
 aaaaaaaa aaaaaaaaaa 4148

(210) 55
 (211) 414
 (212) PRT
 (213) Homo sapiens

(400) 55
 Met Ser Gly Leu Asp Gly Gly Asn Lys Leu Pro Leu Ala Gln Thr Gly
 1 5 10 15
 Gly Leu Ala Ala Pro Asp His Ala Ser Gly Asp Pro Asp Leu Asp Gln
 20 25 30
 Cys Gln Gly Leu Arg Glu Glu Thr Glu Ala Thr Gln Val Met Ala Asn
 35 40 45
 Thr Gly Gly Gly Ser Leu Glu Thr Val Ala Glu Gly Gly Ala Ser Gln
 50 55 60
 Asp Pro Val Asp Cys Gly Pro Ala Leu Arg Val Pro Val Ala Gly Ser
 65 70 75 80
 Arg Gly Gly Ala Ala Thr Lys Ala Gly Gln Glu Asp Ala Pro Pro Ser

(400) 55
 Met Ser Gly Leu Asp Gly Gly Asn Lys Leu Pro Leu Ala Gln Thr Gly
 1 5 10 15

130	135	140
Pro Gly Lys Lys Ala Lys Glu Val Thr Thr Lys Lys Arg Ala Ile Ser		
145	150	155 160
Ala Ala Val Glu Lys Glu Gly Glu Ala Gly Ala Ala Met Glu Glu Lys		
	165	170 175
Lys Val Val Gln Lys Glu Lys Lys Val Ala Gly Gly Val Lys Glu Glu		
	180	185 190
Thr Arg Pro Arg Ala Pro Lys Ile Asn Asn Cys Met Asp Ser Leu Glu		
	195	200 205
Ala Ile Asp Gln Glu Leu Ser Asn Val Asn Ala Gln Ala Asp Arg Ala		
	210	215 220
Phe Leu Gln Leu Glu Arg Lys Phe Gly Arg Met Arg Arg Leu His Met		
	225	230 235 240
Gln Arg Arg Ser Phe Ile Ile Gln Asn Ile Pro Gly Phe Trp Val Thr		
	245	250 255
Ala Phe Arg Asn His Pro Gln Leu Ser Pro Met Ile Ser Gly Gln Asp		
	260	265 270
Glu Asp Met Leu Arg Tyr Met Ile Asn Leu Glu Val Glu Glu Leu Lys		
	275	280 285
His Pro Arg Ala Gly Cys Lys Phe Lys Phe Ile Phe Gln Gly Asn Pro		
	290	295 300
Tyr Phe Arg Asn Glu Gly Leu Val Lys Glu Tyr Glu Arg Arg Ser Ser		
	305	310 315 320
Gly Arg Val Val Ser Leu Ser Thr Pro Ile Arg Trp His Arg Gly Gln		
	325	330 335
Asp Pro Gln Ala His Ile His Arg Asn Arg Glu Gly Asn Thr Ile Pro		
	340	345 350
Ser Phe Phe Asn Trp Phe Ser Asp His Ser Leu Leu Glu Phe Asp Arg		
	355	360 365
Ile Ala Glu Ile Ile Lys Gly Glu Leu Trp Ile Asn Ile Leu Gln Tyr		
	370	375 380
Tyr Leu Met Gly Glu Gly Pro Arg Arg Gly Ile Arg Gly Pro Pro Arg		
	385	390 395 400
Gln Pro Val Glu Ser Ala Arg Ser Phe Arg Phe Gln Ser Gly		
	405	410

<222> (1) (801)

<400> 56

ctg aaa ggg ggg agg ccc agg gtg gtg aac tcc acc tgc agt gac ttc	48
Leu Lys Gly Ala Arg Pro Arg Val Val Asn Ser Thr Cys Ser Asp Phe	
1 5 10 15	
aac cat ggc tca gct ctg cac atc gct gcc tgc aat ctg tgc ctg ggc	96
Asn His Gly Ser Ala Leu His Ile Ala Ala Ser Asn Leu Cys Leu Gly	
20 25 30	
gcc gcc aaa tgt tta ctg gag cat ggt gcc aac cca ggc ctg agg aat	144
Ala Ala Lys Cys Leu Leu Glu His Gly Ala Asn Pro Ala Leu Arg Asn	
35 40 45	
cga aaa gga cag gta cca ggc gaa gtg gtc cca gac cca atg gac atg	192
Arg Lys Gly Gln Val Pro Ala Glu Val Val Pro Asp Pro Met Asp Met	
50 55 60	
tcc ctt gat aag gca gag gca gcc ctg gly gcc aag gaa ttg cgg atg	240
Ser Leu Asp Lys Ala Glu Ala Ala Leu Val Ala Lys Glu Leu Arg Thr	
65 70 75 80	
ctg cta gaa gag gct gtg cca ctg tcc tgc acc ctt cct aaa gtc aca	288
Leu Leu Glu Glu Ala Val Pro Leu Ser Cys Thr Leu Pro Lys Val Thr	
85 90 95	
cta ccc aat tat gac aac gtc cca ggc aat ctc atg ctc agc ggc ctg	336
Leu Pro Asn Tyr Asp Asn Val Pro Gly Asn Leu Met Leu Ser Ala Leu	
100 105 110	
ggc ctg cgt cta gga gac cga gtg ctc ctc gat gcc cag aag acg ggt	384
Gly Leu Arg Leu Gly Asp Arg Val Leu Leu Asp Gly Gln Lys Thr Gly	
115 120 125	
acg ctg agg ttc tgc ggg acc acc gag ttc gcc agt gcc cag tgg gtc	432
Thr Leu Arg Phe Cys Gly Thr Thr Glu Phe Ala Ser Gly Gln Trp Val	
130 135 140	
ggc gtg gag cta gat gaa cgg gaa gcc aag aac gac gcc agc gtt gcc	480
Gly Val Glu Leu Asp Glu Pro Glu Gly Lys Asn Asp Gly Ser Val Gly	
145 150 155 160	
gtg gta cgt tac ttc atc tgc ctt att aag cgt gtt gta ttt gta ttt	528
Gly Val Asn Tyr Phe Ile Cys Pro Ile Lys Gln Gly Leu Ile Ala Ser	
165 170 175	
gtg tcc aag gtc tcc aag gca gtg gat gca ccc ccc tca tct gtt acc	576
Val Ser Lys Val Ser Lys Ala Val Asp Ala Pro Pro Ser Ser Val Thr	
180 185 190	
tcc aag ccc cgt act ccc cgt atg gac ttc tcc gct gta aac ggc aaa	624

ctg gta cgt tac ttc atc tgc ctt att aag cgt gtt gta ttt gta ttt
Gly Val Asn Tyr Phe Ile Cys Pro Ile Lys Gln Gly Leu Ile Ala Ser

gtg gta cgt tac ttc atc tgc ctt att aag cgt gtt gta ttt gta ttt

225

230

235

240

caa gtc att gtg gca ggc cag aac agg gat tgt ggg ttt cta tgg gaa 764
Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
245 250 255

gac aga att tgc tcc agg tta ctg gta tgg cat tgaactggac cagcccacgg 801
Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
260 265

gcaagcatga cggctctgtg ttgggtgtcc ggtactttac ctgtgccccg aggcacgggg 841

tctttgcacc agcatcttgt atccagagga ttgggtggatc cactgatccc cctggagaca 941

gtgttgggagc aaaaaaagtg catcaagtga caatgacaca gcccaaacgc accttcacaa 1041

cagtccggac cccaaaggac attgcacacg agaactctat ctccagggtt ctctctctgt 1081

gtcgttttcc ttggatgtgt agggcgggaga tgcagtctta gagacctgga tacctgacac 1121

agagacagag tccctctctag catctctctga cacaaggaga cccagtcac cctaagatag 1161

agattcccag tgacacctcc agaatagaaa ccccgtttagc cagccctcga ttaactgaggt 1241

cccattatta acagatctcc catgaagcct ccccaaaata cagacctcat gttaccccaa 1341

aagagattcc ctgagttagca ccttcaggtt agtccctgtc cctacccct cagagcagat 1381

ttcccccatt aaacattttc cacatcacc cagggtatgt gacccctccc accacaggac 1441

gtctctgagt taccagtggg ttagagtccc atgaatgaag acccccccba ccccggttct 1481

ccttaagcat aggtccatacc tccagaatag ccagccacat cactatcccc atgtaacata 1541

agtctcctca aaatggcgtg aggtccactag aaagacctta tactctcttc tctttctcag 1601

agatgccttc catcaactta agtccctgtt ctcacccctg aacaagacac ctaattaacc 1661

ggcccactca cctcaattac aaacaccaaa atcgtcctgg aagcatgaat tacaggacag 1721

caagtcttcc tgcctctctg acccttgaga aacccccagt gccttggtatg aagcccaccc 1781

ccatgccc acagtccctg tcttgcccaa ggtccacaga aaattctctt tctttcaag 1841

taattctt cccctctt ggggtatcc caatttga gactcttc tagaacctg 1901

gggagttcaa attccagaga gaatatatat tatatataat ccccaattcc ccatgcttcc 1961

aagccctaca atctctagaa gaccccaaat ttctaattcc caggacttcc cctaccccaag 2021

taattctt cccctctt ggggtatcc caatttga gactcttc tagaacctg 2081

taattctt cccctctt ggggtatcc caatttga gactcttc tagaacctg 2141

taattctt cccctctt ggggtatcc caatttga gactcttc tagaacctg 2201

taattctt cccctctt ggggtatcc caatttga gactcttc tagaacctg 2261

attcaatata cctctgggtc acagggtosaa gacartaat ctgagtcatt ggccccaaag 2441
 gacttcacag caactgggoc agactaacag cctgagggag aactgaggg ccccggtgggt 2501
 ccagagcaga cctggggccc tgaccaccaa ggaagctca cgaactgccc ttcactgat 2561
 gtccctaacc tcagcatgac tctgtctc ttaataaag acgtttctat ggcaaaaaaa 2621
 aaaaaaaaaa aaaaaaaaaa aa 2643

<210> 57
 <211> 267
 <212> PRT
 <213> Rattus sp.

<400> 57

Leu	Lys	Gly	Ala	Arg	Pro	Arg	Val	Val	Asn	Ser	Thr	Cys	Ser	Asp	Phe
1				5					10					15	
Asn	His	Gly	Ser	Ala	Leu	His	Ile	Ala	Ala	Ser	Asn	Leu	Cys	Leu	Gly
		20						25					30		
Ala	Ala	Lys	Cys	Leu	Leu	Glu	His	Gly	Ala	Asn	Pro	Ala	Leu	Arg	Asn
		35				40						45			
Arg	Lys	Gly	Gln	Val	Pro	Ala	Glu	Val	Val	Pro	Asp	Pro	Met	Asp	Met
	50					55					60				
Ser	Leu	Asp	Lys	Ala	Glu	Ala	Ala	Leu	Val	Ala	Lys	Glu	Leu	Arg	Thr
	65				70					75				80	
Leu	Leu	Glu	Glu	Ala	Val	Pro	Leu	Ser	Cys	Thr	Leu	Pro	Lys	Val	Thr
		85							90					95	
Leu	Pro	Asn	Tyr	Asp	Asn	Val	Pro	Gly	Asn	Leu	Met	Leu	Ser	Ala	Leu
		100						105					110		
Gly	Leu	Arg	Leu	Gly	Asp	Arg	Val	Leu	Leu	Asp	Gly	Gln	Lys	Thr	Gly
	115						120					125			
Thr	Leu	Arg	Ile	Cys	Gly	Thr	Thr	Glu	Phe	Ala	Ser	Gly	Gln	Trp	Val
	130					135						140			
Gly	Val	Gln	Leu	Arg	Glu	Pro	Ala	Gly	Lys	Asn	Arg	Gly	Ser	Val	Gly
	145				150					155				160	
Gly	Val	Arg	Tyr	Phe	Ile	Cys	Pro	Pro	Lys	Gln	Gly	Leu	Phe	Ala	Ser
		165							170				175		
Val	Ser	Lys	Val	Ser	Lys	Ala	Val	Asp	Ala	Pro	Pro	Ser	Ser	Val	Thr

Gly Arg Arg Val His Lys Gly Lys Lys Lys Arg Trp Arg Ser Trp Arg
 180 185 190 195 200 205 210 215 220 225

225

10

133

24

Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
 245 250 255

Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
260 265

```

<210> 58
<211> 2929
<212> DNA
<213> Rattus sp.

```

- (2.20)•
- (2.21)• CDS
- (2.22)• (1) .. (310)

04400-58
ggt gaa tct acc tct aga tgg got gag gcc atc aga gaa atc tct ggt 48
Ala Asp Ser Thr Ser Arg Trp Ala Glu Ala Leu Arg Glu Ile Ser Gly
 5 10 15

cgt tta gct gaa atg cct gca gat agt gga tac cct gca tac ctt ggt 96
Arg Leu Ala Glu Met Pro Ala Asp Ser Gly Tyr Pro Ala Tyr Leu Gly
 20 25 30

gct cga ctg gct tct ttc tat gag cga gca ggc aga gtg aaa tgt ctt 144
 Ala Arg Leu Ala Ser Phe Tyr Glu Arg Ala Gly Arg Val Lys Cys Leu
 35 40 45

Gga uac cct gag aga gaa ggg agt gtc agc att gta gga gca gtt tct 192
 Gly Asn Pro Glu Arg Glu Gly Ser Val Ser Ile Val Gly Ala Val Ser
 50 55 60

cca cct ggt ggt gat ttt tct gat cca gtc aca tct gct act ctg ggt 240
 Pro Pro Gly Gly Asp Phe Ser Asp Pro Val Thr Ser Ala Thr Leu Gly
 61 70 75 80

att gtt cag gtg ttc tgg ggc ttg gat aag aag cta gct cag cgc aag 283
Ile Val Gln Val Phe Trp Gly Leu Asp Lys Lys Leu Ala Gln Arg Lys
35 90 95

[illegible]

gac ctg gac gag tac tat gac aaa cac ttc aca gag ttc gtg cct ctg 384
Ala Leu Asp Glu Tyr Tyr Asp Lys His Phe Thr Glu Phe Val Pro Leu
115 120 125

agg acc aaa ggt aag gag att ctg cag gaa gag gag gat ctg qcg gaa 432

165 170 175
 ggg tac aac cct tat gac agg ttc tgt cca ttc tac aag aag gtg ggg 576
 Gly Tyr Thr Pro Tyr Asp Arg Phe Cys Pro Phe Tyr Lys Thr Val Gly
 180 185 190
 atg ctg tcc aac atg att tca ttc tat gat atg gcc cgc cgg gct gtg 624
 Met Leu Ser Asn Met Ile Ser Phe Tyr Asp Met Ala Arg Arg Ala Val
 195 200 205
 gag aac aac gcc cag agt gac aat aag atc aca tgg tcc att atc cgt 672
 Glu Thr Thr Ala Gln Ser Asp Asn Lys Ile Thr Trp Ser Ile Ile Arg
 210 215 220
 gag cac atg ggg gag att ctc tat aaa ctt tcc tcc atg aaa ttc aag 720
 Glu His Met Gly Glu Ile Leu Tyr Lys Leu Ser Ser Met Lys Phe Lys
 225 230 235 240
 gat cca gtg aag gat gcc gag gca aag atc aag gcc gac tac gca cag 768
 Asp Pro Val Lys Asp Gly Glu Ala Lys Ile Lys Ala Asp Tyr Ala Gln
 245 250 255
 ctt ctt gaa gat atg cag aac gca ttc cgt agc ctg gaa gat 810
 Leu Leu Glu Asp Met Gln Asn Ala Phe Arg Ser Leu Glu Asp
 260 265 270
 tagaactgtg aactctctcc tctctctccg cagctcatat gtgtatatatt tcttgaattt 870
 ctcatctcca accctttgct tccatattgt gcagctttga gactagtgcg tegtqcggtc 930
 tegtctattt tctgttttct ttggtagggtc ttataaaaaca cacattcctg tctctcgctg 990
 tctgaaggag ctcttgacct ttgtctgaag tgggtgaatgt agtgcatatg atacacagtg 1050
 taacatacac attgtaacat atagctttctg taaacttgta tgtaagggtga ctaccccttc 1110
 cctctctccc agtaaaactgt aaacaggact actgcatgtg ctctattggg gatggaaggc 1170
 cagatctcca taccgtggac aggtacataa ggaaaactaga ccaacttgcaa cttagtgttt 1230
 gttgagtaac cattttgcag gaagtatttc catttaaaaa acaaaaagatt aatgttccaa 1290
 ctattgtac ctctcagat atcaatcag actgtttgtg aggcacttg gaaatttt 1350
 gtttctca agacgttg caggttga agtaatagat aattcagtt cttt gaaa 1410
 tgtgaaagta aaaagadagc taggtgggtc gaattaaatt gacatcgtct tgttaagca 1470
 tattttattt cactgagaga tttaatatca aggaatttta tatactcaat tactaggaaa 1530
 tctttctca agcaatttt aattctatt aaacttga tctctctt aatttttt 1590
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 1650
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 1710
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 1770
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 1830
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 1890
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 1950
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2010
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2070
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2130
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2190
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2250
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2310
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2370
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2430
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2490
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2550
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2610
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2670
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2730
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2790
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2850
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2910
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 2970
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3030
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3090
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3150
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3210
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3270
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3330
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3390
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3450
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3510
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3570
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3630
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3690
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3750
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3810
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3870
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3930
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 3990
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4050
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4110
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4170
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4230
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4290
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4350
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4410
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4470
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4530
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4590
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4650
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4710
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4770
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4830
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4890
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 4950
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5010
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5070
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5130
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5190
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5250
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5310
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5370
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5430
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5490
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5550
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5610
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5670
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5730
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5790
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5850
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5910
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 5970
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6030
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6090
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6150
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6210
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6270
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6330
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6390
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6450
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6510
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6570
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6630
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6690
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6750
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6810
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6870
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6930
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 6990
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7050
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7110
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7170
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7230
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7290
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7350
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7410
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7470
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7530
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7590
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7650
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7710
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7770
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7830
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7890
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 7950
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8010
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8070
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8130
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8190
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8250
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8310
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8370
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8430
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8490
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8550
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8610
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8670
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8730
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8790
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8850
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8910
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 8970
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9030
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9090
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9150
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9210
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9270
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9330
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9390
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9450
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9510
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9570
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9630
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9690
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9750
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9810
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9870
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9930
 ctgtttttt cttttttt cttttttt cttttttt cttttttt cttttttt 9990

aaagaaaaaa aagatogatt ttgtgtttgc tgttttgggt tgtttaaata ataatcccat 1950
 atttgcataa cgaggtctgc ttctgagaga ttggagatcg tctccctctt tcaactctcg 2010
 ggggtgataat gctgggggca tctacccctt tcaggagggg aaggggattg aacatggcta 2070
 acaactctca gtaacacaagc gtaacgacaa agtattttatt ttaagccctg gtatgtttgt 2130
 taaattatta ggtgggtgat ttcttatggt ctcttgggta gacatagtat acaactcaga 2190
 tctaatgtgt aaatccctgc tagtgcatgt ctacacgata gactgctatt caagaaggat 2250
 attcttcacg ataacaattt aaaaactatt aaacagata tggattatgc aatgacttgt 2310
 tgagaggttg attaacgggt ctgcttaata agtttgcctt caatatggct tctatccag 2370
 aagccctgac tagtggagat gagaaagatt tcaaaaacct tctgcctaca cctaccagca 2430
 acctagggtt gtgacagaa tgaatgctcc caagaaaata ctggaccagc tctgttttgt 2490
 tctccctgat ttgagatgtg cgttctctct cctctcgaga ctgttgatgt atgagtgtga 2550
 agaagttaca gaaacaacgc tcagattttc acggtaactt tccctctgcc cacactgtag 2610
 agttccagat tcttcaactg tagtgcttct ttctgaagga tctgttaaaa tatagcagtc 2670
 tttttaaagc attatgcagt tctctattta ttgtgctgtg cctgggtcta agtgcagccg 2730
 gttaaaacag ttccatatgt atttttccag tgttaaatct catacctatg ccttttgga 2790
 agctccatcc tgaacaatga atagaagagg ctatataaat tgcctcctta tcttaagat 2850
 tccactatct ttatgttaag agtaatgtat aattattaaa atctatgaaa aataaaaagt 2910
 ggatttaaat taagagatc 2929

<210> 59
 <211> 270
 <212> PRT
 <213> Rattus sp.

<400> 59
 Ala Asp Ser Thr Ser Arg Trp Ala Met Ala Leu Arg Ala Ile Ser Gly
 1 10
 Arg Leu Ala Glu Met Pro Ala Asp Ser Gly Tyr Pro Ala Tyr Leu Gly
 20 25 30
 Ala Arg Leu Ala Ser Phe Tyr Glu Arg Ala Gly Arg Val Lys Cys Leu
 35 40 45

111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

His Phe Pro Ser Val Asn Trp Leu Ile Ser Tyr Ser Lys Tyr Met Arg
 100 105 110
 Ala Leu Asp Glu Tyr Tyr Asp Lys His Phe Thr Glu Phe Val Pro Leu
 115 120 125
 Arg Thr Lys Ala Lys Glu Ile Leu Gln Glu Glu Glu Asp Leu Ala Glu
 130 135 140
 Ile Val Gln Leu Val Gly Lys Ala Ser Leu Ala Glu Thr Asp Lys Ile
 145 150 155 160
 Thr Leu Glu Val Ala Lys Leu Ile Lys Asp Asp Phe Leu Gln Gln Asn
 165 170 175
 Gly Tyr Thr Pro Tyr Asp Arg Phe Cys Pro Phe Tyr Lys Thr Val Gly
 180 185 190
 Met Leu Ser Asn Met Ile Ser Phe Tyr Asp Met Ala Arg Arg Ala Val
 195 200 205
 Glu Thr Thr Ala Gln Ser Asp Asn Lys Ile Thr Trp Ser Ile Ile Arg
 210 215 220
 Glu His Met Gly Glu Ile Leu Tyr Lys Leu Ser Ser Met Lys Phe Lys
 225 230 235 240
 Asp Pro Val Lys Asp Gly Glu Ala Lys Ile Lys Ala Asp Tyr Ala Gln
 245 250 255
 Leu Leu Glu Asp Met Gln Asn Ala Phe Arg Ser Leu Glu Asp
 260 265 270

<210> 60
 <211> 1489
 <212> DNA
 <213> Rattus sp.

<220>
 <221> CDS
 <222> (1)..(1453)

<400> 1
 gca att tta cag gaa agc gag cat gaa gaa gag gag gag gaa gaa gaa 45
 Ala Arg Leu Pro Ala Pro Glu His Ala Arg Gln Gln Pro Leu Leu Ser
 1 5 10 15
 ggc cat gag gaa gga tag taa gaa gga att gaa att gaa gga gaa gaa 26
 Gly Pro His Pro His Ser Ser Ala Arg Val Pro Val Pro Gly Val Ala
 20 25 30

att tta att gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa 37
 Glu Arg His His His His Arg His His His His His His His His His

ggg ctc cac cgc cag tct gga agg gtt cca cat acg gga agg gcc tac 240
 Gly Leu His Arg Gln Ser Gly Arg Val Pro His Thr Gly Thr Ala Tyr
 65 70 75 80

ttc gca gat gag ccc acc gag gct cag gct ccg ggc gga ttc tgc gtg 288
 Phe Ala Asp Glu Pro Thr Glu Ala Gln Ala Pro Gly Gly Phe Cys Val
 85 90 95

tca ccc tgg ctc ctt ggg gtc cgc tgg ccg gcc tgt gcc acc cgg acg 336
 Ser Pro Ser Leu Leu Gly Val Arg Trp Pro Ala Cys Ala Thr Arg Thr
 100 105 110

ccc gga tca ctg cct ctg tct ccc cca tca ggc cag ccc cgg acg cta 384
 Pro Gly Ser Leu Pro Leu Ser Pro Pro Ser Ala Gln Pro Arg Thr Leu
 115 120 125

tgg ccc acc cct cca gct ggc ccc tgg agt agg atg gta gca cgt aac 432
 Trp Pro Thr Pro Pro Ala Gly Pro Ser Ser Arg Met Val Ala Arg Asn
 130 135 140

cag gtg gca gcc gac aat gag atc tcc ccg gca tca gag ccc cga cgg 480
 Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala Ser Glu Pro Arg Arg
 145 150 155 160

cgg cca gag cca tcc tgg tcc tgg tct tgg tcc tgg ccg ggc gcc ccg 528
 Arg Pro Glu Pro Ser Ser Ser Ser Ser Ser Ser Pro Ala Ala Pro
 165 170 175

gag cgt ccc cgg ccc tgc cca gtg gtc cca gcc ccg gct cca ggc gac 576
 Ala Arg Pro Arg Pro Cys Pro Val Val Pro Ala Pro Ala Pro Gly Asp
 180 185 190

act cac ttc cgc acc ttc cgc tcc cac tct gat tac cgg cgt atc acg 624
 Thr His Phe Arg Thr Phe Arg Ser His Ser Asp Tyr Arg Arg Ile Thr
 195 200 205

cgg acc agc gct ctc ctg gac gcc tgc ggc ttc tac tgg gga ccc ctg 672
 Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe Tyr Trp Gly Pro Leu
 210 215 220

agc gtg cat ggg ggc cac gaa cgg ctg cgt gcc gag ccc gtg ggc acc 720
 Ser Val His Gly Ala His Glu Arg Leu Arg Ala Glu Pro Val Gly Thr
 225 230 235 240

ttc tgg tgg cga ggc ggc agt cct tgg tgg cca ttc ttc ttc ttc agt 768
 Phe Leu Val Arg Arg Ser Arg Val Arg Asn Tyr Ile Ile Ala Leu Ser
 245 250 255

gtg aag atg gct tgg ggc ccc aag agc att cgt gtg cag ttc cag gcc 816
 Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg Val His Phe Gln Ala
 260 265 270

ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 864
 Phe Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350

Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln Gln Leu Cys Arg Gln
 305 310 315 320
 cgc atc gtg gcc gcc gtg ggt cgc gag aac ctg gca cgc atc cct ctt 1208
 Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu Ala Arg Ile Pro Leu
 325 330 335
 aac cgc gta ctc cgt gac tac ctg agt tcc ttc ccc ttc cag atc 1253
 Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe Pro Phe Gln Ile
 340 345 350
 tgaagggtg ccgcggtgcc ccgagcatta agtgggagcg ccttattatt tcttattatt 1313
 attattatt attttttctgg aacacgtgg gaggcctccc cgcctaggtc ggagggagtg 1373
 ggtgggagg gtgagatgcc tcccacttct ggctggagac cttatccgcg ctctcggggg 1433
 gctccccc ctggtgctcc ctcgcgggcc ccttggttgt agcagcttgt gtctggggcc 1493
 aggaactgaa ctcacagcct accctcccat gtttacatgt tcccagtatc ttgacacaaa 1553
 ccaggggtgg gggaggggtct ctggcttcat tttctgtgt tgcagaatat tctattttat 1613
 attttacat ccagtttaga taataaacct tattatgaaa gttttttttt taaagaaaaa 1673
 aaaaaaaaa aaaaaa 1733

<110> 61
 <111> 361
 <112> PRT
 <213> Rattus sp.

<400> 61
 Ala Arg Leu Pro Ala Pro Glu His Ala Arg Gln Gln Pro Leu Leu Ser
 1 5 10 15
 Gly Pro Glu Pro Gly Ser Ser Ala Arg Val Pro Val Pro Gly Val Ala
 20 25 30
 Ser Arg Arg Gln Pro Arg Gly Gly Lys Pro Pro Ser Gly Asp Gly Leu
 35 40 45
 Glu Ser Gly Pro Ser Pro Arg Pro Leu Leu His Ala Arg Gly Glu Ala
 50 55 60
 Gly Leu His Arg Gln Ser Gly Arg Val Pro His Thr Gly Thr Ala Tyr
 65 70 75 80
 Phe Ala Asp Glu Pro Thr Glu Ala Gln Ala Pro Gly Gly Phe Cys Val
 85 90 95

Seq ID: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1367, 1368, 1369, 1370, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518, 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536, 1537, 1538, 1539, 1540, 1541, 1542, 1543, 1544, 1545, 1546, 1547, 1548, 1549, 1550, 1551, 1552, 1553, 1554, 1555, 1556, 1557, 1558, 1559, 1560, 1561, 1562, 1563, 1564, 1565, 1566, 1567, 1568, 1569, 1570, 1571, 1572, 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 1581, 1582, 1583, 1584, 1585, 1586, 1587, 1588, 1589, 1590, 1591, 1592, 1593, 1594, 1595, 1596, 1597, 1598, 1599, 1600, 1601, 1602, 1603, 1604, 1605, 1606, 1607, 1608, 1609, 1610, 1611, 1612, 1613, 1614, 1615, 1616, 1617, 1618, 1619, 1620, 1621, 1622, 1623, 1624, 1625, 1626, 1627, 1628, 1629, 1630, 1631, 1632, 1633, 1634, 1635, 1636, 1637, 1638, 1639, 1640, 1641, 1642, 1643, 1644, 1645, 1646, 1647, 1648, 1649, 1650, 1651, 1652, 1653, 1654, 1655, 1656, 1657, 1658, 1659, 1660, 1661, 1662, 1663, 1664, 1665, 1666, 1667, 1668, 1669, 1670, 1671, 1672, 1673, 1674, 1675, 1676, 1677, 1678, 1679, 1680, 1681, 1682, 1683, 1684, 1685, 1686, 1687, 1688, 1689, 1690, 1691, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1699, 1700, 1701, 1702, 1703, 1704, 1705, 1706, 1707, 1708, 1709, 1710, 1711, 1712, 1713, 1714, 1715, 1716, 1717, 1718, 1719, 1720, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729, 1730, 1731, 1732, 1733, 1734, 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1742, 1743, 1744, 1745, 1746, 1747, 1748, 1749, 1750, 1751, 1752, 1753, 1754, 1755, 1756, 1757, 1758, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1766, 1767, 1768, 1769, 1770, 1771, 1772, 1773, 1774, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1783, 1784, 1785, 1786, 1787, 1788, 1789, 1790, 1791, 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 1802, 1803, 1804, 1805, 1806, 1807, 1808, 1809, 1810, 1811, 1812, 1813, 1814, 1815, 1816, 1817, 1818, 1819, 1820, 1821, 1822, 1823, 1824, 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838, 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848, 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1857, 1858, 1859, 1860, 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1870, 1871, 1872, 1873, 1874, 1875, 1876, 1877, 1878, 1879, 1880, 1881, 1882, 1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931, 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 207

Journal of Management Inquiry 18(6) 709–724
© The Author(s) 2009
Reprints and permissions:
<http://www.sagepub.com/journalsPermissions.nav>

tag tac tag cag gag gcc cag gag cgt acc cgg cca tgc cag gta gta 267
 Ser Ser Ser Pro Ala Ala Pro Ala Arg Pro Arg Pro Cys Pro Val Val
 35 40 45

cag gcc cag gat cag ggc gac act caa ttc cgg acc ttc cgg tcc caa 315
 Pro Ala Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His
 50 55 60

tct gat tac cgg cgg att acg cgg acc agc gct ctg ctg gac gcc tgc 363
 Ser Asp Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys
 65 70 75

ggc ttc tac tgg gga cca ctg agc gtg cat ggg ggg cca gaa cgg ctg 411
 Gly Phe Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu
 80 85 90

cgt gcc gag ccc gtg ggc acc ttc ttg gtg cgc gac agt cgg cag cgg 459
 Arg Ala Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg
 95 100 105 110

aac tgc ttc ttc gcg ctg agc gtg aag atg gct tgc ggc cca acg agc 507
 Asn Cys Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser
 115 120 125

att cgt gtg caa ttc caa gcc ggc cgc ttc caa ctg gac gcc agc cgc 555
 Ile Arg Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg
 130 135 140

gag acc ttc gag tgc ctg ttc gag ctg ctg gag caa tac gtg gcg gcc 603
 Glu Thr Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala
 145 150 155

cgg cgc cgc atg ttg ggc gcc cca ctg cgc cag cgc cgc gtg cgg cgg 651
 Pro Arg Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro
 160 165 170

ctg cag gag ctg tgt cgc cag cgc atc gtg gcc gcc gtg ggt cgc gag 699
 Leu Gln Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu
 175 180 185 190

aac ctg gca cgc atc cct ctt aac cgg gta ctg cgt gac tac ctg agt 747
 Asn Leu Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser
 195 200 205

tgc ttc ccc ttc caa att caa att caa att caa att caa att caa att 795
 Ser Phe Pro Phe Gln Ile
 210

agtgggaggg cattattatt cattattatt aattattatt attttttcgg aacacgggg 855
 gggattttt gggaggga gggggggtt gttggggtt gggagatgac taacatttt 915

tattatgaaa gttttttttt taaaaaadaaa aaaaaaaa

1194

<210> 63
<211> 212
<212> IRT
<213> Rattus sp.

<400> 63
Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala
1 5 10 15
Ser Glu Pro Arg Arg Arg Pro Glu Pro Ser Ser Ser Ser Ser Ser Ser
20 25 30
Ser Pro Ala Ala Pro Ala Arg Pro Arg Pro Cys Pro Val Val Pro Ala
35 40 45
Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ser Asp
50 55 60
Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe
65 70 75 80
Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala
85 90 95
Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys
100 105 110
Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg
115 120 125
Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr
130 135 140
Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg
145 150 155 160
Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln
165 170 175
Gln Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu
180 185 190
Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Ile Ser Ser Pro
195 200 205
Pro Phe Gln Ile
210

<210> 63

<400> 64

```

cttccaaaga ctgcagagccc ttagggccca ggtttcaaca gattcttcaa a atg cca 57
                                         Met Pro
                                         1

tcc caa atg gag cat gcc atg gaa acc atg atg ett aca ttt cac agg 105
Ser Gln Met Glu His Ala Met Glu Thr Met Met Leu Thr Phe His Arg
      5                      10                      15

ttt caa ggg gaa aaa aac tac ttg aca aag gag gac ctg aga gtg ctc 153
Phe Ala Gly Glu Lys Asn Tyr Leu Thr Lys Glu Asp Leu Arg Val Leu
      20                      25                      30

atg gaa agg gag ttc cct ggg ttt ttg gaa aat caa aag gac cct ctg 201
Met Glu Arg Glu Phe Pro Gly Phe Leu Glu Asn Gln Lys Asp Pro Leu
      35                      40                      45                      50

gct gtg gac aaa ata atg aaa gac ctg gac cag tgc cga gat gga aaa 249
Ala Val Asp Lys Ile Met Lys Asp Leu Asp Gln Cys Arg Asp Gly Lys
      55                      60                      65

gtg ggc ttc cag agc ttt cta tca cta gtg ggc ggc ctc atc att gca 297
Val Gly Phe Gln Ser Phe Leu Ser Leu Val Ala Gly Leu Ile Ile Ala
      70                      75                      80

tgc aat gac tat ttt gta gta cac atg aag cag aag aag taggccaact 346
Cys Asn Asp Tyr Phe Val Val His Met Lys Gln Lys Lys
      85                      90                      95

ggagccctgg taacacacac ttgatgggtc ctctcccatg ggttcaactg aggaatctgc 406

cccactgctt cctgtgagca gatcaggacc cttaggaaat gtgcaataa catccaactc 466

caattcgaca agcagagaaa gaaaagttaa tccaatgaca gaggagcttt cgagtittat 526

attgtttgca tcgggttgcc ctcaataaag aaagtctttt tttttaagtt ccgaaaaaaaa 586

aaaaaaaaaa aaaa 600

```

<210> 65

<211> 95

<212> FRT

<213> Rattus sp.

<410> 67

```

Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met Met Leu Thr Phe
      1                      5                      10                      15

```

```

His Arg Phe Ala Gly Glu Lys Asn Tyr Leu Thr Lys Glu Asp Leu Arg
      20                      25                      30

```

```

cttccaaaga ctgcagagccc ttagggccca ggtttcaaca gattcttcaa a atg cca

```

```

tcc caa atg gag cat gcc atg gaa acc atg atg ett aca ttt cac agg

```

Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys Gln Lys Lys
 85 90 95

(210> 66
 (211> 639
 (212> DNA
 (213> Rattus sp.

(220>
 (221> CDS
 (222> (1)..(636)

(400> 66
 atg gcg tac gcc tat ctc ttc aag tac atc atc atc ggc gac aca ggt 48
 Met Ala Tyr Ala Tyr Leu Phe Lys Tyr Ile Ile Ile Gly Asp Thr Gly
 1 5 10 15
 gtt ggt aaa tgg tgc tta ttg cta cag ttt aca gac aag agg ttt cag 96
 Val Gly Lys Ser Cys Leu Leu Leu Gln Phe Thr Asp Lys Arg Phe Gln
 20 25 30
 ccu gtg cat gac ctc aca att ggt gta gag ttt ggt gct cga atg ata 144
 Pro Val His Asp Leu Thr Ile Gly Val Gln Phe Gly Ala Arg Met Ile
 35 40 45
 acc att gat ggg aaa cag ata aaa ctc cag atc tgg gat aca gca ggg 192
 Thr Ile Asp Gly Lys Gln Ile Lys Leu Gln Ile Trp Asp Thr Ala Gly
 50 55 60
 cag gag tcc ttt cgt tct atc aca agg tca tat tac aga ggt gca ggc 240
 Gln Gln Ser Phe Arg Ser Ile Thr Arg Ser Tyr Tyr Arg Gly Ala Ala
 65 70 75 80
 ggg gct tta cta gtc tat gat att aca agg aga gac acg ttc aac cac 288
 Gly Ala Leu Leu Val Tyr Asp Ile Thr Arg Arg Asp Thr Phe Asn His
 85 90 95
 ttg aca acc tgg tta gaa gac gcc cgt cag cat tcc aat tcc aac atg 336
 Leu Thr Thr Trp Leu Glu Asp Ala Arg Gln His Ser Asn Ser Asn Met
 100 105 110
 gtc atc atg ctt att gga aat aaa agt gac tta gaa tct agg aga gaa 384
 Val Ile Met Leu Ile Gly Asn Lys Ser Asp Leu Gln Ser Arg Arg Gln
 115 120 125
 gtg aaa aag gaa gaa ggt gaa gct ttt gca cga gag cat gga ctt atc 432
 Val Lys Lys Glu Glu Gly Glu Ala Phe Ala Arg Glu His Gly Leu Ile
 130 135 140
 ttc atc gaa act ttc ttc aat att ttc tct aat tta tta tta tta tta 480
 Phe Met Glu Thr Ser Ala Lys Thr Ala Ser Asn Val Glu Glu Ala Phe
 145 150 155 160 165 170 175 180 185 190 195

atg atc atc atc atc atc atc atc atc atc atc atc atc atc atc atc 520
 Arg Ile Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg

gac acc aat gca tct cac gga ggc aac caa gga ggg cag cag gca ggg 624
 Ala Thr Asn Ala Ser His Gly Gly Asn Gln Gly Gly Gln Gln Ala Gly
 195 200 205

gga ggc tgc tgc tga 639
 Gly Gly Cys Cys
 210

<210> 67
 <211> 212
 <212> PRT
 <213> Rattus sp.

<400> 67
 Met Ala Tyr Ala Tyr Leu Phe Lys Tyr Ile Ile Ile Gly Asp Thr Gly
 1 5 10 15

Val Gly Lys Ser Cys Leu Leu Leu Gln Phe Thr Asp Lys Arg Phe Gln
 20 25 30

Pro Val His Asp Leu Thr Ile Gly Val Glu Phe Gly Ala Arg Met Ile
 35 40 45

Thr Ile Asp Gly Lys Gln Ile Lys Leu Gln Ile Trp Asp Thr Ala Gly
 50 55 60

Gln Glu Ser Phe Arg Ser Ile Thr Arg Ser Tyr Tyr Arg Gly Ala Ala
 65 70 75 80

Gly Ala Leu Leu Val Tyr Asp Ile Thr Arg Arg Asp Thr Phe Asn His
 85 90 95

Leu Thr Thr Trp Leu Glu Asp Ala Arg Gln His Ser Asn Ser Asn Met
 100 105 110

Val Ile Met Leu Ile Gly Asn Lys Ser Asp Leu Glu Ser Arg Arg Glu
 115 120 125

Val Lys Lys Glu Glu Gly Glu Ala Phe Ala Arg Glu His Gly Leu Ile
 130 135 140

Phe Met Glu Thr Ser Ala Lys Thr Ala Ser Asn Val Glu Glu Ala Phe
 145 150 155 160

Ile Asn Thr Ala Lys Glu Ile Tyr Glu Lys Ile Gln Glu Gly Val Phe
 165 170 175

Asp Ile Asn Asn Glu Ala Asn Gly Ile Lys Ile Gly Pro Gln His Ala
 180 185 190

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (1) ... (813)

<400> 68

```

atg gtg ctg ctc aag gaa tat cgg gtc atc ctg cct gtg tct gta gat      48
Met Val Leu Leu Lys Glu Tyr Arg Val Ile Leu Pro Val Ser Val Asp
   1             5             10             15

gag tat caa gtg ggg cag ctg tac tct gtg gct gaa gcc agt aaa aat      96
Glu Tyr Gln Val Gly Gln Leu Tyr Ser Val Ala Glu Ala Ser Lys Asn
          20             25             30

gaa act ggt ggt ggg gaa ggt gtg gag gtc ctg gtg aac gag ccc tac      144
Glu Thr Gly Gly Gly Gln Gly Val Glu Val Leu Val Asn Glu Pro Tyr
          35             40             45

gag aag gat gat ggc gag aaa ggc cag tac aca cac aag atc tac cac      192
Glu Lys Asp Asp Gly Gln Lys Gly Gln Tyr Thr His Lys Ile Tyr His
          50             55             60

tta cag agc aaa gtt ccc aag ttt gtt cga atg ctg gcc cca gaa ggc      240
Leu Gln Ser Lys Val Pro Thr Phe Val Arg Met Leu Ala Pro Glu Gly
          65             70             75

gcc ctg aat ata cat gag aaa gcc tgg aat gcc tac cct tac tgc aga      288
Ala Leu Asn Ile His Glu Lys Ala Trp Asn Ala Tyr Pro Tyr Cys Arg
          85             90             95

acc gtt att aca aat gag tac atg aag gaa gac ttt ctc att aaa att      336
Thr Val Ile Thr Asn Glu Tyr Met Lys Glu Asp Phe Leu Ile Lys Ile
          100            105            110

gaa acc tgg cac aag cca gac ctt ggc acc cag gag aat gtg cat aaa      384
Glu Thr Trp His Lys Pro Asp Leu Gly Thr Gln Glu Asn Val His Lys
          115            120            125

ctg gag cct gag gca tgg aaa cat gtg gaa gct ata tat ata gac atc      432
Leu Glu Pro Glu Ala Trp Lys His Val Glu Ala Ile Tyr Ile Asp Ile
          130            135            140

tta tta tta atg tta tta tta tta tta tta tta tta tta tta tta tta      480
Ala Asp Arg Ser Gln Val Leu Ser Lys Asp Tyr Lys Ala Gln Glu Asp
          145            150            155            160

cca gca aaa ttt aaa tct atc aaa aca gga cga gga cca ttg ggc cgg      528
Pro Ala Lys Phe Lys Ser Ile Lys Thr Gly Arg Gly Pro Leu Gly Pro
          165            170            175

atg ttt gtt tta tta tta tta tta tta tta tta tta tta tta tta tta      576
Met Lys Val Val Val Val Val Val Val Val Val Val Val Val Val Val
          180            185            190            195

```

Lys Val Glu Asn Phe Ile His Lys Gln Glu Lys Arg Leu Phe Thr Asn
 210 215 220

tat cac agg cag ctg ttc tgt tgg ctt gat aaa tgg gtt gat ctg act 720
 Phe His Arg Gln Leu Phe Cys Trp Leu Asp Lys Trp Val Asp Leu Thr
 225 230 235 240

atg gat gac att cgg agg atg gaa gaa gag acg aag aga cag ctg gat 768
 Met Asp Asp Ile Arg Arg Met Glu Glu Glu Thr Lys Arg Gln Leu Asp
 245 250 255

gag atg aga caa aag gac ccc gtg aaa gga atg aca gca gat gac tag 816
 Glu Met Arg Gln Lys Asp Pro Val Lys Gly Met Thr Ala Asp Asp
 260 265 270

(Q10): 69

(Q11): 2263

(Q12): DNA

(Q13): Simian sp.

(Q400): 69

cgtctctctc ctccccttctc tctagcagta gcctctcttaa tctagcttaa tggctttaca 60

aagaaagcca ggcagaggag cactctctcag tggctgtggt cggacctga cctagctgac 120

catgaacttg gaagggcttg aaatgatagc agttctgacg gtcattgtgc tttctgttaa 180

atatttgga cagtttgggc tgattgaagc aggtttagaa gacagcgttg aagatgaact 240

ggagatggcc atgtctagggc atgggcctga ggccttgag cttctggaag ccagagacca 300

attaccaag aaagagcttc agatccttta cagaggattt aagaacgaat gcccagtg 360

tgttgtaaat gaagaaacct tcaaagagat ttactcagc ttctttccac agggagactc 420

tacaacatat gcacatttctc tgttcaatgc gtttgatacg gaccacaatg gagctgtgag 480

tttcgaggat ttcacaaag gtctttccat ttctctcggg gggacagtac aagaaaaact 540

caattgggca tttaatctgt atgatataaa taaagatggc tacatcaact aagaggaaat 600

gttgatata atgaaagca atctgacat gatgggtaaa tgaatatac atgtctctca 660

atgctatgca atgagcaat atctgacat atctctctca atctctctca atctctctca 720

tggtgtgtgt acatagatg agttcattga aagctgcaaa aaagatgaaa acataatg 780

ctccatgcag ctctttgaaa atgtgattta acttgctaac tagatcctga atccaaaga 840

aaatgtgaa ctctctctca atctctctca atctctctca atctctctca atctctctca 900

atctctctca atctctctca atctctctca atctctctca atctctctca atctctctca 960

atctctctca atctctctca atctctctca atctctctca atctctctca atctctctca 1020

atctctctca atctctctca atctctctca atctctctca atctctctca atctctctca 1080

taatataactg acatctgcac ttaatttcca gaaattaaat taattctcat gcttgaatga 1260
 tctaattcca tttatatact ttaagtaaac aaataagatt actacaatta aagacatagt 1320
 tcaagtttct atggccttca ctcccccctt tctattagaa attaatctta tctgggtattt 1380
 ttaaacattt aaaaattttat catcagatat cagcatatgc ctaattatgc ctaatgaaac 1440
 ttaataagca ttttaatttc catcatacat tatagtcagc gcttatatac tatatataat 1500
 ttgggatttg ttttaatttc caggtctggtt tccattgtat catcaagtgg aagttcaaga 1560
 cggcatcaaa caaaaacaagg atgtttacag acatatgcaa aggttcagga tatctatcct 1620
 ccagtatatg ttaatgotta ataacaagta atctaacag cattaaaggc caaatctgtc 1680
 ctcttccccc tgacttctt acagcatggt tatattacaa gccattcagg gacaaagaaa 1740
 ccttgaactac cccactgtct actaggaaca aacaaacagc aagcaaaatt cactttgaac 1800
 gcaccagtggt ttcattaca ttgacaaact ctaccaagat tcagtagaaa ataagtgtct 1860
 aacaaactaat ccagattaca atatgattta gtgcacata aaattccaac aattcagatt 1920
 atttttaact aactcagcca caactgtaaa gttgccacat tactaaagac acacacatcg 1980
 tccctgtttt gttagaaatat caaaaagacc aagaggtcac agaaggagga aatttgcaac 2040
 tgtctttgca acaataaact aggtatctat tctggtgtag agataggatg ttgaaagctg 2100
 cctgtctatc accagtgtag aaattaagag tagtacaata catgtacact gaaatttgcc 2160
 atcgctgttt tgtgtaaaat caatgtgcac attttgtatt tcaaaaagaa aaaataaaa 2220
 aaaaataaaa tgtttataac tctaaaaaaa aaaaaaaaaa aaa 2280

(210> 70
 (211> 229
 (212> PRT
 (213> Simian sp.

(400> 70
 Met Asn Leu His Gly Leu His Met Ile Ala Val Leu Ile Val Ile Val
 1 5 10
 Leu Phe Val Lys Leu Leu Glu Gln Phe Gly Leu Ile Glu Ala Gly Leu
 20 25 30

His Arg Ser Val Glu Asp Gln Leu Ala Met Ala Thr Val Arg His Arg
 35 40

(410> 70
 Met Asn Leu His Gly Leu His Met Ile Ala Val Leu Ile Val Ile Val
 1 5 10

85

90

95

Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp
100 105 110

Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe Ile Lys Gly Leu
115 120 125

Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys Leu Asn Trp Ala Phe
130 135 140

Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met
145 150 155 160

Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly Lys Cys Thr Tyr
165 170 175

Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val Glu Thr Phe Phe
180 185 190

Gln Lys Met Asp Lys Asn Lys Asp Gly Val Val Thr Ile Asp Glu Phe
195 200 205

Ile Glu Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu
210 215 220

Phe Glu Asn Val Ile
225

(210) 71
(211) 2259
(212) DNA
(213) Simian sp.

(400) 71
gtcgacagac gccctggccc ggtggactcc tgagtcttac tcttgacccc tgcgtcccca 60
gacagaatg tgaggagagt ggaaagcatt tcggtccagc tggaggaggc cagctccaca 120
ggcgutttcc tgtatgctca gaacagcacc aagcgcagca tttaaagagcg gctcatgaag 180
ctcttgcctt gtcagctgc caaaacatcg tctctctta ttcaaacag cgtggagat 240
tcttggga tctctctgt tctctctct tctctctct tctctctct tctctctct 300
agcaaatcta caaagaaaga gcttcagatc cttacagag gatttaagaa cgaatgcctc 360
agtgggtgtg ttaatgaaga aaccttcaaa gagatttaac cgcagttctt tccacaggga 420
gactctaaaa catatgcaca tttctctct tctctctct tctctctct tctctctct 480
tctctctct tctctctct tctctctct tctctctct tctctctct tctctctct 540

gctctctct tctctctct tctctctct tctctctct tctctctct tctctctct 600
tctctctct tctctctct tctctctct tctctctct tctctctct tctctctct 660
tctctctct tctctctct tctctctct tctctctct tctctctct tctctctct 720
tctctctct tctctctct tctctctct tctctctct tctctctct tctctctct 780
tctctctct tctctctct tctctctct tctctctct tctctctct tctctctct 840
tctctctct tctctctct tctctctct tctctctct tctctctct tctctctct 900

atggggttca tggaggttct tgaatatgtg atttaatttg tcaactagat cctgaatcca 840
 acagacaaat gtgaactatt ctaccacct taaagtccga gctaccactt ttagcataga 900
 ttgtctagct tgacactgaa goataattat gaaacaagct ttgttttaat ataaagcaat 960
 ccccaaaaga tttagatttc taagttataa atttgcaccc ttccataat gccactgagt 1020
 tcattgggatg ttctgactca ttccatactc tgtgaatatt caaaagtaat agaattctggc 1080
 atatagtttt attgatttct tagcatggg attattgagg ctttcacata taagtcatct 1140
 taaaatacca gtgttttttg ctactcattt gctatgtatc agtcttagga ttttgaatgg 1200
 tttctcaata tactgacac tgcatttaat ttccagaaat taaattaatt ttcattgtctg 1260
 aatgtctgaa ttccatttat atactttaag taaacaaata agattactac aattaaacac 1320
 atagttccag tttctatggc cttcacttcc cactttctat tagaaattaa ttttatctgg 1380
 tatttttaaa catttaaaaa ttatcatca gataccgca tatgcctaatt tatgcctaatt 1440
 gaaacttaat aagcatttaa tttccatca tacattatag tcaaggcata tatactatat 1500
 ataattttgg atttgtttta tcttacaggc tgttttccat tgtatcatca agtggaagtt 1560
 caagaaggca tcaaacaaaa caaggatggt tacagacata tgcaaaaggt caggatatct 1620
 atctctcagt atatgttaat gcttaataac aagtaactct aacagcatta aaggccaaat 1680
 ctgtctctct cccctgact ccttacagc atgttttat tataagccat tcagggaaca 1740
 agaaacottg actacccac tgtctactag gaacaaacaa acagcaagca aaattcactt 1800
 tgaagcacc agtgggttca ttacattgac aactactacc aagattcagt agaaaataag 1860
 tgcacaacaa ctaatccaga ttacaatat atttagtgc caataaaatt ccaacaatto 1920
 agattatttt taatcacctc agccacaaat gtaaagttgc cacattacta aagacacaca 1980
 catcgtccct gttttgtaga aatacacaa agaccaagag gctacagaag gagaaaaatt 2040
 ccaactgtct ttgcaaat aattaggtc tctattctg tctgacata gctattca 2100
 agttctctc tctacaaat tttacaaat ccttctctc tctattctg tctgacata 2160
 ttgccatggc gtgtttgtgt aaactcaatg tgcacatttt gtatttcaaa aagaaaaaat 2220
 aaaagcaaaa taaaatgtta aaaaaaaaaa aaaaaaaa 2280

2280

2280

2280

2280

Ser Ser Thr Gly Gly Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser
 20 25 30
 Ile Lys Glu Arg Leu Met Lys Leu Leu Pro Cys Ser Ala Ala Lys Thr
 35 40 45
 Ser Ser Pro Ala Ile Gln Asn Ser Val Glu Asp Glu Leu Glu Met Ala
 50 55 60
 Thr Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser
 65 70 75 80
 Lys Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn
 85 90 95
 Glu Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr
 100 105 110
 Ser Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu
 115 120 125
 Phe Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp
 130 135 140
 Phe Ile Lys Gly Leu Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys
 145 150 155 160
 Leu Asn Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile
 165 170 175
 Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met
 180 185 190
 Gly Lys Cys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His
 195 200 205
 Val Glu Thr Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Val Val
 210 215 220
 Thr Ile Asp Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn Ile Met
 225 230 235 240
 Arg Ser Met Gln Leu Phe Glu Asn Val Ile
 245 250

<210> 73

<211> 11

<212> FRT

<213> Simian sp.

<400> 73

Ser Asn Ala Lys Ala Val Glu Thr Asp Val
 1 15